

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2003, 09:09:19 ; Search time 15 Seconds  
(without alignments)  
653.189 Million cell updates/sec

Title: US-09-593-288-2

Perfect score: 1731  
Sequence: 1 SSKGKRRNPGLIKIPKEAFE.....TLHESKGTDVASFVKLLGD 333

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database :

- 1: Issued Patents AA.\*
- 2: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/6C.COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 1731  | 100.0       | 334    | 1  | US-08-530-950-4   |
| 2          | 1731  | 100.0       | 334    | 3  | US-08-576-240-2   |
| 3          | 1731  | 100.0       | 334    | 4  | US-08-888-429A-4  |
| 4          | 1731  | 100.0       | 334    | 4  | US-09-149-879-4   |
| 5          | 1367  | 79.0        | 318    | 4  | US-08-888-429A-2  |
| 6          | 1359  | 78.5        | 318    | 4  | US-08-530-950-2   |
| 7          | 1359  | 78.5        | 318    | 4  | US-09-149-879-2   |
| 8          | 1358  | 78.5        | 318    | 4  | US-08-446-083-2   |
| 9          | 919   | 53.1        | 333    | 4  | US-08-888-429A-8  |
| 10         | 919   | 53.1        | 333    | 4  | US-08-530-950-10  |
| 11         | 919   | 53.1        | 333    | 2  | US-08-874-186-92  |
| 12         | 919   | 53.1        | 333    | 4  | US-08-888-429A-10 |
| 13         | 919   | 53.1        | 333    | 4  | US-09-149-879-10  |
| 14         | 916.5 | 52.9        | 363    | 4  | US-08-530-950-6   |
| 15         | 916.5 | 52.9        | 363    | 4  | US-08-888-429A-6  |
| 16         | 916.5 | 52.9        | 363    | 4  | US-09-149-879-6   |
| 17         | 906   | 52.3        | 333    | 1  | US-08-530-950-8   |
| 18         | 906   | 52.3        | 333    | 4  | US-08-888-429A-8  |
| 19         | 833   | 48.1        | 185    | 4  | US-09-149-879-8   |
| 20         | 698   | 40.3        | 333    | 4  | US-09-384-162-11  |
| 21         | 697   | 40.3        | 333    | 4  | US-08-888-429A-21 |
| 22         | 694   | 40.1        | 389    | 4  | US-09-446-754-2   |
| 23         | 694   | 40.1        | 419    | 4  | US-08-888-429A-20 |
| 24         | 694   | 40.1        | 419    | 4  | US-08-888-429A-28 |
| 25         | 694   | 40.1        | 468    | 4  | US-09-446-754-6   |
| 26         | 690.5 | 39.9        | 453    | 4  | US-09-446-754-4   |
| 27         | 687   | 39.7        | 468    | 4  | US-08-888-429A-32 |

|    |       |      |     |   |                   |                   |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 685   | 39.6 | 380 | 4 | US-08-888-429A-30 | Sequence 30, Appl |
| 29 | 683.5 | 39.5 | 346 | 4 | US-08-888-429A-18 | Sequence 18, Appl |
| 30 | 609.5 | 35.2 | 367 | 4 | US-08-888-429A-13 | Sequence 13, Appl |
| 31 | 606   | 35.0 | 668 | 1 | US-08-530-950-13  | Sequence 13, Appl |
| 32 | 606   | 35.0 | 668 | 4 | US-09-149-879-13  | Sequence 13, Appl |
| 33 | 600   | 34.7 | 405 | 4 | US-08-888-429A-22 | Sequence 22, Appl |
| 34 | 587   | 33.9 | 393 | 1 | US-08-888-429A-33 | Sequence 33, Appl |
| 35 | 587   | 33.9 | 393 | 4 | US-08-530-950-11  | Sequence 11, Appl |
| 36 | 587   | 33.9 | 393 | 4 | US-08-888-429A-11 | Sequence 11, Appl |
| 37 | 587   | 33.9 | 393 | 4 | US-09-149-879-11  | Sequence 11, Appl |
| 38 | 583   | 33.7 | 400 | 2 | US-08-878-988-17  | Sequence 17, Appl |
| 39 | 583   | 33.7 | 400 | 4 | US-09-272-796-17  | Sequence 17, Appl |
| 40 | 579   | 33.4 | 267 | 2 | US-07-857-224B-37 | Sequence 37, Appl |
| 41 | 566   | 32.7 | 400 | 4 | US-08-530-950-12  | Sequence 12, Appl |
| 42 | 566   | 32.7 | 400 | 4 | US-09-149-879-12  | Sequence 12, Appl |
| 43 | 563   | 32.5 | 400 | 4 | US-08-888-429A-12 | Sequence 12, Appl |
| 44 | 557   | 32.2 | 400 | 2 | US-08-878-988-3   | Sequence 3, Appl  |
| 45 | 557   | 32.2 | 400 | 4 | US-09-272-796-3   | Sequence 3, Appl  |

ALIGNMENTS

RESULT 1  
US-08-530-950-4  
Sequence 4, Application US/08530950  
Patent No. 5736381  
GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Ralondeau, Joel  
APPLICANT: Gupta, Shashi  
APPLICANT: Derjard, Benoit  
TITLE OF INVENTION: CYTOKINE-, AND  
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESS: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/530,950  
FILING DATE: 19-SEP-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/010001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 334 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
US-08-530-950-4  
Query Match 100.0% Score 1731; DB 1; Length 334;  
Best Local Similarity 100.0% Pred. No. 2.2e-165;  
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 SSKGKRRNPGLIKIPKEAFEQPTSTPRDLSKACISIGNONFEVKADDEPTIELGR 60

Db 2 SOSKCKRNPGLIKIRKEAFEPQSTSPRDLDSKACISIGNONFEVKADDELPIMELGR 61  
QY 61 GAYGVKMRHVPSSQIMAVKRIRATVNSQEQKRLMDLDSMRVDCPFTVTFYGALEFR 120  
Db 62 GAYGVKMRHVPSSQIMAVKRIRATVNSQEQKRLMDLDSMRVDCPFTVTFYGALEFR 121  
QY 121 EGDVWICMELMDTSLDKFYKQYIDKGQTIPEDLIGIAVSIVKALEHLSKLSVYHRDVK 180  
Db 122 EGDVWICMELMDTSLDKFYKQYIDKGQTIPEDLIGIAVSIVKALEHLSKLSVYHRDVK 181  
QY 181 PSNVLINALGOVKMCDGFSIGYLVDVAKTIDAGCKPYMAPERINPELNOKGYSVKSIDW 240  
Db 182 PSNVLINALGOVKMCDGFSIGYLVDVAKTIDAGCKPYMAPERINPELNOKGYSVKSIDW 241  
QY 241 SLGITMIELALIRFPYDSWGTTPFOOLKQVVEEPPSLPADKFSAEFVDFTSOCLKKNSE 300  
Db 242 SLGITMIELALIRFPYDSWGTTPFOOLKQVVEEPPSLPADKFSAEFVDFTSOCLKKNSE 301  
QY 301 RPTYPELMQHFFFTLHESKGTDVASFVKILIGD 333  
Db 302 RPTYPELMQHFFFTLHESKGTDVASFVKILIGD 334

RESULT 2  
US-08-576-240-2  
Sequence 2, Application US/08576240  
Patent No. 6074862  
GENERAL INFORMATION:  
APPLICANT: Stein, Bernd  
APPLICANT: Yang, Maria  
TITLE OF INVENTION: MITOGEN-ACTIVATED PROTEIN KINASE KINASE  
TITLE OF INVENTION: MEK6 AND METHODS OF USE THEREFOR  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/576,240  
FILING DATE: 20-DEC-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 860098.403  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 334 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-576-240-2

Query Match 100.0%; Score 1731; DB 3; Length 334;  
Best Local Similarity 100.0%; Pred. No. 2.2e-165;  
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOSKCKRNPGLIKIRKEAFEPQSTSPRDLDSKACISIGNONFEVKADDELPIMELGR 60  
Db 2 SOSKCKRNPGLIKIRKEAFEPQSTSPRDLDSKACISIGNONFEVKADDELPIMELGR 61

QY 61 GAYGVKMRHVPSSQIMAVKRIRATVNSQEQKRLMDLDSMRVDCPFTVTFYGALEFR 120  
Db 62 GAYGVKMRHVPSSQIMAVKRIRATVNSQEQKRLMDLDSMRVDCPFTVTFYGALEFR 121  
QY 121 EGDVWICMELMDTSLDKFYKQYIDKGQTIPEDLIGIAVSIVKALEHLSKLSVYHRDVK 180  
Db 122 EGDVWICMELMDTSLDKFYKQYIDKGQTIPEDLIGIAVSIVKALEHLSKLSVYHRDVK 181  
QY 181 PSNVLINALGOVKMCDGFSIGYLVDVAKTIDAGCKPYMAPERINPELNOKGYSVKSIDW 240  
Db 182 PSNVLINALGOVKMCDGFSIGYLVDVAKTIDAGCKPYMAPERINPELNOKGYSVKSIDW 241  
QY 241 SLGITMIELALIRFPYDSWGTTPFOOLKQVVEEPPSLPADKFSAEFVDFTSOCLKKNSE 300  
Db 242 SLGITMIELALIRFPYDSWGTTPFOOLKQVVEEPPSLPADKFSAEFVDFTSOCLKKNSE 301  
QY 301 RPTYPELMQHFFFTLHESKGTDVASFVKILIGD 333  
Db 302 RPTYPELMQHFFFTLHESKGTDVASFVKILIGD 334

RESULT 3  
US-08-888-429A-4  
Sequence 4, Application US/08888429A  
Patent No. 6136596  
GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Whitmarsh, Alan  
APPLICANT: Tourlier, Cathy  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-  
TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/888,429A  
FILING DATE: 07-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/530,950  
FILING DATE: 19-SEP-1995  
APPLICATION NUMBER: 08/446,083  
FILING DATE: 19-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fassg, Peter J.  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/053001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 334 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-08-888-429A-4

Query Match 100.0%; Score 1731; DB 4; Length 334;  
Best Local Similarity 100.0%; Pred. No. 2.2e-165;  
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOSKGRKRNPGIKIKPEAFEPQOTSTPPRDLDSKACISIGNONFEVKADDEPIEIMELGR 60  
Db 2 SOSKGRKRNPGIKIKPEAFEPQOTSTPPRDLDSKACISIGNONFEVKADDEPIEIMELGR 61  
QY 61 GAYGVEKRRHVPSSQIMAVKRIATVNSOEQRLLMDLISMRVDCPFTVYFYGALFR 120  
Db 62 GAYGVEKRRHVPSSQIMAVKRIATVNSOEQRLLMDLISMRVDCPFTVYFYGALFR 121  
QY 121 EGDVWICMELMDTSLDKFYKQVIDKGQTIPEIDILGKIAVSIVKALEHLHSKLSVYHRDVK 180  
Db 122 EGDVWICMELMDTSLDKFYKQVIDKGQTIPEIDILGKIAVSIVKALEHLHSKLSVYHRDVK 181  
QY 181 PSNVILNALGVKMCDFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 240  
Db 182 PSNVILNALGVKMCDFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 241  
QY 241 SLGITMIELALIRFPYDSWGTPEQOLKQVVEEPPQLPADKFSAEFVDFTSOCLKKNKSKE 300  
Db 242 SLGITMIELALIRFPYDSWGTPEQOLKQVVEEPPQLPADKFSAEFVDFTSOCLKKNKSKE 301  
QY 301 RPTYPELMQHPPFTLHESKGTDVASFVKLLIGD 333  
Db 302 RPTYPELMQHPPFTLHESKGTDVASFVKLLIGD 334

## RESULT 4

US-09-149-879-4  
Sequence 4, Application US/09149879

GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Raingeaud, Joel  
APPLICANT: Gupta, Shashi  
APPLICANT: Derjard, Benoit  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/149,879  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/530,950  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/010001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 334 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear

US-09-149-879-4

Query Match 100.0%; Score 1731; DB 4; Length 334;  
Best Local Similarity 100.0%; Pred. No. 2,2e-165;  
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOSKGRKRNPGIKIKPEAFEPQOTSTPPRDLDSKACISIGNONFEVKADDEPIEIMELGR 60  
Db 2 SOSKGRKRNPGIKIKPEAFEPQOTSTPPRDLDSKACISIGNONFEVKADDEPIEIMELGR 61  
QY 61 GAYGVEKRRHVPSSQIMAVKRIATVNSOEQRLLMDLISMRVDCPFTVYFYGALFR 120  
Db 62 GAYGVEKRRHVPSSQIMAVKRIATVNSOEQRLLMDLISMRVDCPFTVYFYGALFR 121  
QY 121 EGDVWICMELMDTSLDKFYKQVIDKGQTIPEIDILGKIAVSIVKALEHLHSKLSVYHRDVK 180  
Db 122 EGDVWICMELMDTSLDKFYKQVIDKGQTIPEIDILGKIAVSIVKALEHLHSKLSVYHRDVK 181  
QY 181 PSNVILNALGVKMCDFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 240  
Db 182 PSNVILNALGVKMCDFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 241  
QY 241 SLGITMIELALIRFPYDSWGTPEQOLKQVVEEPPQLPADKFSAEFVDFTSOCLKKNKSKE 300  
Db 242 SLGITMIELALIRFPYDSWGTPEQOLKQVVEEPPQLPADKFSAEFVDFTSOCLKKNKSKE 301  
QY 301 RPTYPELMQHPPFTLHESKGTDVASFVKLLIGD 333  
Db 302 RPTYPELMQHPPFTLHESKGTDVASFVKLLIGD 334

## RESULT 5

US-08-888-429A-2  
Sequence 2, Application US/08888429A

GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Whitmarsh, Alan  
APPLICANT: Tournier, Cathy  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-  
TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE KINASES  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/888,429A  
FILING DATE: 07-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/530,950  
FILING DATE: 19-SEP-1995  
APPLICATION NUMBER: 08/446,083  
FILING DATE: 19-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/053001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 299354

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
APPLICANT: Raingeaud, Joel  
APPLICANT: Gupta, Shashi  
APPLICANT: Derlyard, Benolt  
TITLE OF INVENTION: CYCLOKINE-, STRESS-, AND  
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
TITLE OF INVENTION: KINASES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/530,950  
FILING DATE: 19-SEP-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/010001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ. ID NO.: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 318 amino acids

[illegible]

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
84





CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/782,482  
 FILING DATE: 10-JAN-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saxe, Stephen A.  
 REGISTRATION NUMBER: 38,609  
 REFERENCE/DOCKET NUMBER: 24884-121392-01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4848  
 TELEFAX: 202-962-8300  
 INFORMATION FOR SEQ ID NO: 92:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 399 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-874-186-92

Query Match 53.1%; Score 919; DB 2; Length 399;  
 Best Local Similarity 51.3%; Pred. No. 6,6e-84;  
 Matches 181; Conservative 56; Mismatches 92; Indels 24; Gaps 6;

QY 1 SOSGKKR-----NPKLIPKE-----AFEDPQTSTPPRLDLSKACISIG-NQN 44  
 DB 35 SSMGKRRALKLNFPANPFKSTARFTLNPNFTGVONPHIERLRTHSISSGKLIKISPECH 94  
 QY 45 FEVKADLEPIELMELGAGVGVYVERKRVHPSGQIMAVKRIRATVNSOEKRLMDIDISMR 104  
 DB 95 WDFEADLKDGLGELGAGVGVYVERKRVHPSGQIMAVKRIRATVNSOEKRLMDIDISMR 154  
 QY 105 TVDCPTVYTFYFALFREGDVCWICMELMDSIDKFKY--QVIDKGQITPEDIIGKIAVSI 161  
 DB 155 SSDCPYIVQFYFALFREGDVCWICMELMDSIDKFKYKYYVSLD--DVIPETLIGKITLAT 212  
 QY 162 VKALEHLSKLSVTHRDVPSNVNLINALGVYKMGDFGSGIYLVDSVATIDAGCRPYMAP 221  
 DB 213 VKALNHLKENKLTIRHDIKPSNLTLDGSGNKLCDPGLVDSVATIDAGCRPYMAP 272  
 QY 222 ERINPELNQKGSVSKDIMSGLITMELALIRFPYDSMGTPFOOLKQVVEEPPOLPAD- 280  
 DB 273 ERIDPSASRQGYDVRDWSLGLITLVELATGRFPYKPNMSVFDQLTQVVGKDPOLNSNE 332  
 QY 281 --KFSAEVDFTSQCCKNKSKEPTYPPELMQHPFTLHESKGTVDASFYKLL 331  
 DB 333 EREFSPSTINFNVLCLTKDESKRPKYKELKHPIILMYERAVEVACVCKIL 385

# RESULT 12

US-08-888-429A-10  
 Sequence 10, Application US/08888429A  
 Patent No. 6136396  
 GENERAL INFORMATION:  
 APPLICANT: Davis, Roger J.  
 APPLICANT: Whitmarsh, Alan  
 APPLICANT: Tourlier, Cathy  
 TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-  
 TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE  
 NUMBER OF SEQUENCES: 34  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows95  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/888,429A

FILING DATE: 07-JUL-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/530,950  
 FILING DATE: 19-SEP-1995  
 APPLICATION NUMBER: 08/446,083  
 FILING DATE: 19-MAY-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fasse, Peter J.  
 REGISTRATION NUMBER: 32,983  
 REFERENCE/DOCKET NUMBER: 07917/053001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 TELETYPE: 299354  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 399 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: Internal  
 US-08-888-429A-10

Query Match 53.1%; Score 919; DB 4; Length 399;  
 Best Local Similarity 51.3%; Pred. No. 6,6e-84;  
 Matches 181; Conservative 56; Mismatches 92; Indels 24; Gaps 6;

QY 1 SOSGKKR-----NPKLIPKE-----AFEDPQTSTPPRLDLSKACISIG-NQN 44  
 DB 35 SSMGKRRALKLNFPANPFKSTARFTLNPNFTGVONPHIERLRTHSISSGKLIKISPECH 94  
 QY 45 FEVKADLEPIELMELGAGVGVYVERKRVHPSGQIMAVKRIRATVNSOEKRLMDIDISMR 104  
 DB 95 WDFEADLKDGLGELGAGVGVYVERKRVHPSGQIMAVKRIRATVNSOEKRLMDIDISMR 154  
 QY 105 TVDCPTVYTFYFALFREGDVCWICMELMDSIDKFKY--QVIDKGQITPEDIIGKIAVSI 161  
 DB 155 SSDCPYIVQFYFALFREGDVCWICMELMDSIDKFKYKYYVSLD--DVIPETLIGKITLAT 212  
 QY 162 VKALEHLSKLSVTHRDVPSNVNLINALGVYKMGDFGSGIYLVDSVATIDAGCRPYMAP 221  
 DB 213 VKALNHLKENKLTIRHDIKPSNLTLDGSGNKLCDPGLVDSVATIDAGCRPYMAP 272  
 QY 222 ERINPELNQKGSVSKDIMSGLITMELALIRFPYDSMGTPFOOLKQVVEEPPOLPAD- 280  
 DB 273 ERIDPSASRQGYDVRDWSLGLITLVELATGRFPYKPNMSVFDQLTQVVGKDPOLNSNE 332  
 QY 281 --KFSAEVDFTSQCCKNKSKEPTYPPELMQHPFTLHESKGTVDASFYKLL 331  
 DB 333 EREFSPSTINFNVLCLTKDESKRPKYKELKHPIILMYERAVEVACVCKIL 385

# RESULT 13

US-09-149-879-10  
 Sequence 10, Application US/09149879  
 Patent No. 6174676  
 GENERAL INFORMATION:  
 APPLICANT: Davis, Roger J.  
 APPLICANT: Ralugaund, Joel  
 APPLICANT: Gupta, Shashi  
 APPLICANT: Derjard, Benoit  
 TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
 TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/149,879  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/530,950  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fasse, J. Peter  
 REGISTRATION NUMBER: 32,983  
 REFERENCE/DOCKET NUMBER: 07917/010001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 399 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 US-09-149-879-10

Query Match 53.1%; Score 919; DB 4; Length 399;  
 Best Local Similarity 51.3%; Pred. No. 6,6e-84;  
 Matches 181; Conservative 56; Mismatches 92; Indels 24; Gaps 6;

QY 1 SOSKGRK-----NPKLIPKE-----AFEPQSSPPRDLDSKACISIG-NON 44  
 DB 35 SMQGRKRLKLNFAFPPEKSTAFRLNPPTGVQNPHERLRTHTSISSGKLTISPEOH 94  
 QY 45 FEVKADDDPEIMELGAGVGYEKMHRVPSGOIMAYKRIRATVNSOEKRLMDLIDSMR 104  
 DB 95 WFTAEKDLDELIGAGVGYEKMHRVPSGOIMAYKRIRATVNSOEKRLMDLIDSMR 154  
 QY 105 TVDCPTVTYFGLFREGDVMICMELMDISLDFYK---OVIDKQOTIPEDILGKIVSI 161  
 DB 155 SDCPTVYFGLFREGDVMICMELMDISLDFYK---OVIDKQOTIPEDILGKIVSI 212  
 QY 162 VALLEHLKSLVYHNDVPSNVLINALGVKMCDCISGYLVDSVAKTIDAGCPYMAP 221  
 DB 213 VALNHLKSLVYHNDVPSNVLINALGVKMCDCISGYLVDSVAKTIDAGCPYMAP 272  
 QY 222 ERINPELNQKGSVKSIDMSLGTMTLALIRPPYDWSGTPFOOLKQVVEPSPOLPAD- 280  
 DB 273 ERIDPSASRQGYDVRDWSLGTITLALIRPPYDWSGTPFOOLKQVVEPSPOLPAD- 332  
 QY 281 --KFSAEFYDFTSQCCLKNSKERPTYPELMQHPFTLHESKGTIVASFKVLL 331  
 DB 333 EREFSPSFINFVNLCLTKDESKRPKYLKHPFTLHESKGTIVASFKVLL 385

RESULT 14  
 US-08-530-950-6  
 Sequence 6, Application US/08530950  
 Patent No. 5736381  
 GENERAL INFORMATION:  
 APPLICANT: Davis, Roger J.  
 APPLICANT: Raingaud, Joel  
 APPLICANT: Gupta, Shashi  
 APPLICANT: Dejard, Benoit  
 TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
 TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston

STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/530,950  
 FILING DATE: 19-SEP-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fasse, J. Peter  
 REGISTRATION NUMBER: 32,983  
 REFERENCE/DOCKET NUMBER: 07917/010001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 363 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 US-08-530-950-6

Query Match 52.9%; Score 916.5; DB 1; Length 363;  
 Best Local Similarity 54.9%; Pred. No. 1e-83;  
 Matches 175; Conservative 53; Mismatches 82; Indels 9; Gaps 4;

QY 20 EQPQTSSTPPRDLDSKACISIG-NONEVKADDDPEIMELGAGVGYEKMHRVPSGOIM 78  
 DB 33 QNPHERLRTHTSISSGKLTISPEOHWFTAEKDLDELIGAGVGYEKMHRVPSGOIM 92  
 QY 79 AVKRRATVNSOEKRLMDLIDSMRVDCTPTVYFGLFREGDVMICMELMDISLDFYK 138  
 DB 93 AVKRRATVNSOEKRLMDLIDSMRVDCTPTVYFGLFREGDVMICMELMDISLDFYK 152  
 QY 139 YK---OVIDKQOTIPEDILGKIVSIYALVLEHLKSLVYHNDVPSNVLINALGVKMC 195  
 DB 153 YK---OVIDKQOTIPEDILGKIVSIYALVLEHLKSLVYHNDVPSNVLINALGVKMC 210  
 QY 196 DFGISGYLVDSVAKTIDAGCPYMAPERINPELNQKGSVKSIDMSLGTMTLALIRPP 255  
 DB 211 DFGISGYLVDSVAKTIDAGCPYMAPERINPELNQKGSVKSIDMSLGTMTLALIRPP 270  
 QY 256 YDSWGTPTFOOLKQVVEPSPOLPAD---KFSAEFYDFTSQCCLKNSKERPTYPELMQHP 312  
 DB 271 YPKNSVAVDQTLQVYKGPOLNSNEEREFSPSFINFVNLCLTKDESKRPKYLKHPFT 330  
 QY 313 FTLHESKGTIVASFKVLL 331  
 DB 331 ILMYEERAVEVACVCKIL 349

RESULT 15  
 US-08-888-429A-6  
 Sequence 6, Application US/08888429A  
 Patent No. 6136596  
 GENERAL INFORMATION:  
 APPLICANT: Davis, Roger J.  
 APPLICANT: Whitmarsh, Alan  
 APPLICANT: Tounier, Cathy  
 TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-  
 TITLE OF INVENTION: ACTIVATED HUMAN PROTEIN KINASE  
 NUMBER OF SEQUENCES: 34  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA

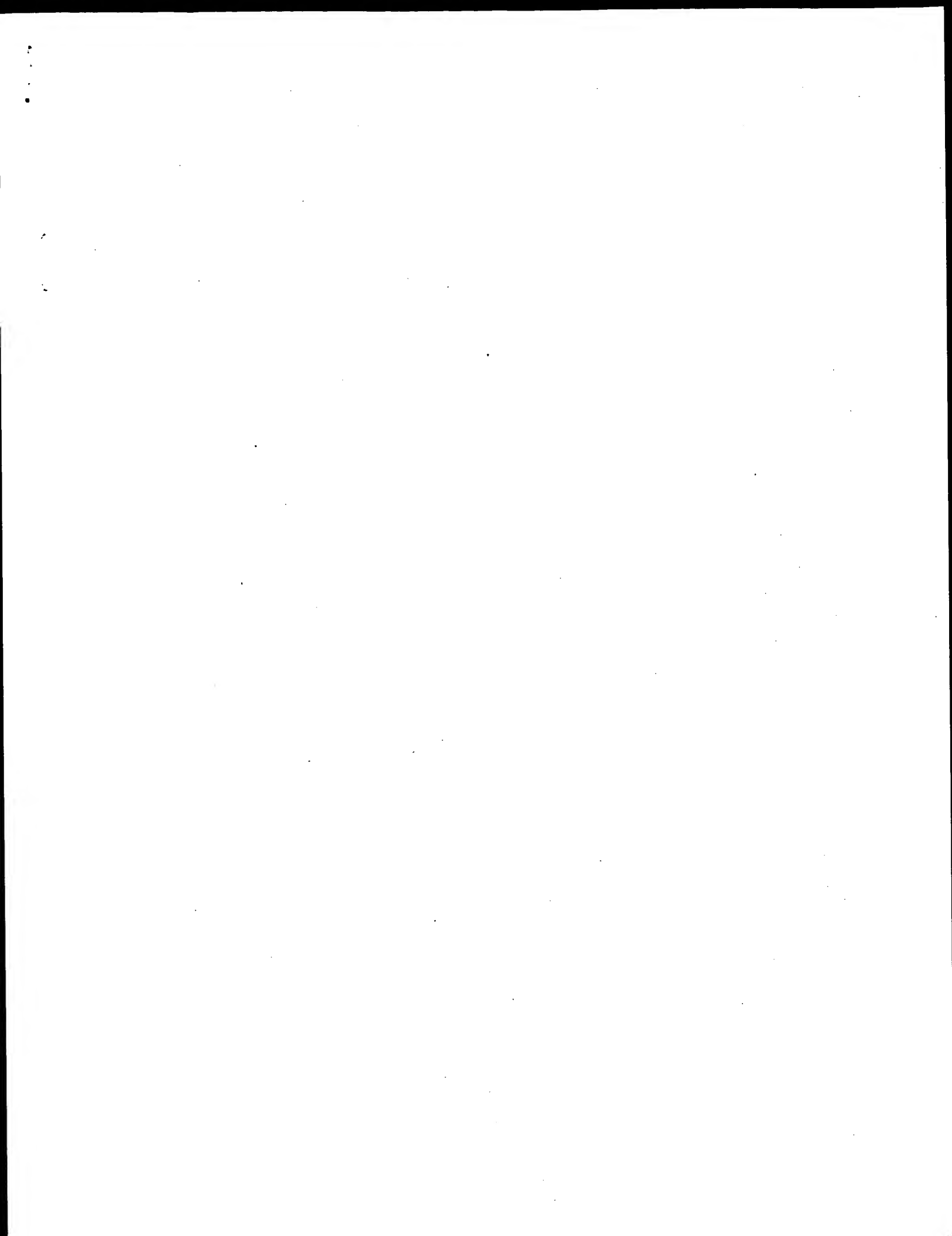


COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/888,429A  
FILING DATE: 07-JUL-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/530,950  
FILING DATE: 19-SEP-1995  
APPLICATION NUMBER: 08/446,083  
FILING DATE: 19-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, Peter J.  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/053001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 299354  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 363 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-888-429A-6

Query Match 52.9%; Score 916.5; DB 4; Length 363;  
Best Local Similarity 54.9%; Pred. No. 1e-83;  
Matches 175; Conservative 53; Mismatches 82; Indels 9; Gaps 4;

QY 20 EOPQTSPPRDLDSKACISIG-NONEVYKADDEPIMELGRGAYGVVEKMRHVPSGQIM 78  
DB 33 QNHIERLRTHSISSGKLIKISPOHMDFTADLDLGEIGRGAYGSVKNVHKPSGQIM 92  
QY 79 AVKRIRATVNSOEQRRLMDDDISMRVDCPFTVTEFGALPREGDWCIMELMDTSLDKF 138  
DB 93 AVKRIRSTVDEKEKQKQLMDLDVYMRSSDCPIYVQFGALPREGDWCIMELMDTSLDKF 152  
QY 139 YK--QVIDKGQITPEDILGRIVASIVKALEHLHSKLSVIRHDKPSNVNLINALGVKKC 195  
DB 153 YKTVYSYLD--DVIPETILGKITLATYKALNHLKENLKIIRHDIKPSNILLDRSGNKKLC 210  
QY 196 DFGISGYVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSDINSLSGITMELATLRFP 255  
DB 211 DFGISQQLVDSIAKTRDAGCRPYMAPERIDPSASROGDVRSVWSLGITLVELATGRFP 270  
QY 256 YDSWGTPFOOLKQVVEEPPQLPAD--KFGAEFVDFTSQCLKKNSKERPTPELMQHPF 312  
DB 271 YPKWNSVFDQLIQVVKDPPQLSNSERERSPSFINFVNLCLTKDSKRPKYKELLKHPF 330  
QY 313 FTIHESKGTDVASFVKLIL 331  
DB 331 IIMYERAVEVACYVCKIL 349

Search completed: June 6, 2003, 09:12:12  
Job time: 17 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2003, 09:11:34 ; Search time 48 Seconds

(without alignments)  
716.229 Million cell updates/sec

Title: US-09-593-288-2

Perfect score: 1731  
Sequence: 1 SOSGKGRNPGLIKPKEAFE.....TLHESKGTDVASFVKLLIGD 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCU\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/PCUUS\_PUBCOMB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 1731  | 100.0       | 334    | 10    | US-09-761-569-4   |
| 2          | 1367  | 79.0        | 318    | 9     | US-09-981-397A-20 |
| 3          | 1367  | 79.0        | 318    | 9     | US-10-059-585-36  |
| 4          | 1359  | 78.5        | 318    | 10    | US-09-761-569-2   |
| 5          | 919   | 53.1        | 399    | 10    | US-09-761-569-10  |
| 6          | 916.5 | 52.9        | 363    | 10    | US-09-761-569-6   |
| 7          | 906   | 52.3        | 393    | 10    | US-09-761-569-8   |
| 8          | 606   | 35.0        | 668    | 9     | US-10-081-119-20  |
| 9          | 606   | 35.0        | 668    | 10    | US-09-761-569-13  |
| 10         | 606   | 35.0        | 668    | 10    | US-09-801-368-238 |
| 11         | 587   | 33.9        | 389    | 10    | US-09-755-665-36  |
| 12         | 587   | 33.9        | 393    | 9     | US-09-918-873-4   |
| 13         | 587   | 33.9        | 393    | 10    | US-09-761-569-11  |
| 14         | 566   | 32.7        | 400    | 10    | US-09-761-569-12  |
| 15         | 563   | 32.5        | 395    | 10    | US-09-755-665-34  |
| 16         | 544   | 31.4        | 364    | 10    | US-09-755-665-64  |
| 17         | 531   | 30.7        | 392    | 10    | US-09-755-665-35  |
| 18         | 531   | 30.7        | 394    | 10    | US-09-755-665-33  |
| 19         | 526   | 30.4        | 380    | 10    | US-09-755-665-8   |

|    |       |      |      |    |                   |                   |
|----|-------|------|------|----|-------------------|-------------------|
| 20 | 502   | 29.0 | 363  | 10 | US-09-755-665-63  | Sequence 63, Appl |
| 21 | 502   | 29.0 | 369  | 10 | US-09-755-665-16  | Sequence 16, Appl |
| 22 | 481   | 27.8 | 515  | 10 | US-09-801-368-384 | Sequence 384, App |
| 23 | 476.5 | 27.5 | 508  | 10 | US-09-801-368-212 | Sequence 212, App |
| 24 | 471   | 27.2 | 346  | 10 | US-09-828-313-36  | Sequence 36, Appl |
| 25 | 471   | 27.2 | 346  | 10 | US-09-828-313-37  | Sequence 37, Appl |
| 26 | 448.5 | 25.9 | 506  | 10 | US-09-801-368-214 | Sequence 214, App |
| 27 | 419   | 24.2 | 487  | 10 | US-09-810-808-8   | Sequence 8, Appl  |
| 28 | 381   | 22.0 | 228  | 10 | US-09-755-665-38  | Sequence 38, Appl |
| 29 | 375   | 21.7 | 1360 | 10 | US-09-871-916-2   | Sequence 2, Appl1 |
| 30 | 370.5 | 21.4 | 1239 | 9  | US-09-291-417-13  | Sequence 13, Appl |
| 31 | 368.5 | 21.3 | 912  | 9  | US-09-291-417-26  | Sequence 26, Appl |
| 32 | 368.5 | 21.3 | 968  | 9  | US-09-291-417-107 | Sequence 107, App |
| 33 | 364.5 | 21.1 | 911  | 9  | US-09-291-417-92  | Sequence 92, Appl |
| 34 | 361   | 20.9 | 1244 | 10 | US-09-755-665-37  | Sequence 37, Appl |
| 35 | 354   | 20.5 | 1244 | 9  | US-09-789-390-13  | Sequence 13, Appl |
| 36 | 354   | 20.5 | 1273 | 9  | US-09-789-390-11  | Sequence 11, Appl |
| 37 | 354   | 20.5 | 1295 | 9  | US-09-789-390-30  | Sequence 30, Appl |
| 38 | 354   | 20.5 | 1295 | 9  | US-09-789-390-32  | Sequence 32, Appl |
| 39 | 354   | 20.5 | 1295 | 9  | US-09-789-390-34  | Sequence 34, Appl |
| 40 | 354   | 20.5 | 1295 | 9  | US-09-789-390-39  | Sequence 39, Appl |
| 41 | 354   | 20.5 | 1303 | 9  | US-09-789-390-39  | Sequence 9, Appl1 |
| 42 | 354   | 20.5 | 1303 | 9  | US-09-789-390-35  | Sequence 35, Appl |
| 43 | 354   | 20.5 | 1303 | 9  | US-09-789-390-38  | Sequence 38, Appl |
| 44 | 354   | 20.5 | 1303 | 9  | US-10-029-115-2   | Sequence 2, Appl1 |
| 45 | 354   | 20.5 | 1312 | 9  |                   |                   |

## ALIGNMENTS

RESULT 1  
US-09-761-569-4  
Sequence 4, Application US/09761569  
Patent No. US20020102691A1  
GENERAL INFORMATION:  
APPLICANT: Davis, Roger J.  
Ratigaund, Joel  
Gupta, Shashi  
Derjard, Benoit  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
KINASES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/761,569  
FILING DATE: 16-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/057,009  
FILING DATE: 1998-04-07  
ATTORNEY/AGENT INFORMATION:  
NAME: Fasse, J. Peter  
REGISTRATION NUMBER: 32,983  
REFERENCE/DOCKET NUMBER: 07917/010001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:

LENGTH: 334 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: No. US20020102691A1 Relevant  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 US-09-761-569-4

Query Match 100.0%; Score 1731; DB 10; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 2e-146;  
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOSGKKRNPGLIKIPKEAFEPQSTSPRRDLDSKACISIGNONFEVKADLEPIEIGR 60  
 DB 2 SOSGKKRNPGLIKIPKEAFEPQSTSPRRDLDSKACISIGNONFEVKADLEPIEIGR 61  
 QY 61 GAYGVEKMRHVPSQIMAVKRIKATVNSQEQKRLMDIDIMRTVDCPTTFYGALFR 120  
 DB 62 GAYGVEKMRHVPSQIMAVKRIKATVNSQEQKRLMDIDIMRTVDCPTTFYGALFR 121  
 QY 121 EGDWICMELMDTSLDKFYKQYIDKQGITPEDILKIAVSIKALEHLSKLSVIRDYK 180  
 DB 122 EGDWICMELMDTSLDKFYKQYIDKQGITPEDILKIAVSIKALEHLSKLSVIRDYK 181  
 QY 181 PSNVILNALGOVKMCDGFSIGYLVDSVAKTIDAGCKPYMAPEIRINELNOKGYSKSDIM 240  
 DB 182 PSNVILNALGOVKMCDGFSIGYLVDSVAKTIDAGCKPYMAPEIRINELNOKGYSKSDIM 241  
 QY 241 SLGITMELALIRFYPYDSMGPPFQOLKOVEEPPOLPADKFSAEFVDTSOCLKKNRSE 300  
 DB 242 SLGITMELALIRFYPYDSMGPPFQOLKOVEEPPOLPADKFSAEFVDTSOCLKKNRSE 301  
 QY 301 RPTYPELMQHPEFTLHESKGTIDVASFVKLLIGD 333  
 DB 302 RPTYPELMQHPEFTLHESKGTIDVASFVKLLIGD 334

RESULT 2  
 US-09-981-397A-20  
 ; Sequence 20, Application US/09981397A  
 ; Publication No. US20030082519A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Axixma Pharmaceuticals AG  
 ; APPLICANT: Schubart, Daniel  
 ; APPLICANT: Habenberger, Peter  
 ; APPLICANT: Stein-Gerlach, Matthias  
 ; APPLICANT: Bevec, Dorian  
 ; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their  
 ; FILE REFERENCE: AXM-004.1 US  
 ; CURRENT FILING DATE: 2002-06-28  
 ; PRIOR APPLICATION NUMBER: 60/240,750  
 ; PRIOR FILING DATE: 2000-10-16  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 20  
 ; LENGTH: 318  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-981-397A-20

Query Match 79.0%; Score 1367; DB 9; Length 318;  
 Best Local Similarity 82.7%; Pred. No. 5.4e-114;  
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;

QY 22 POTSSTPRDLDSKACISIGNONFEVKADLEPIEIMELGAGYGVKMRHVPSQIMAVK 81  
 DB 5 PAPNPTPRNDLSRFTITIGDRNEVEADDLVITISLGRGAGYGVKMRHVPSQIMAVK 64  
 QY 82 RIRATVNSQEQKRLMDIDIMRTVDCPTTFYGALFRGADWICMELMDTSLDKFYKQ 141  
 DB 65 RIRATVNSQEQKRLMDIDIMRTVDCPTTFYGALFRGADWICMELMDTSLDKFYKQ 124

QY 142 VIDKGTIPEDILKIAVSIKALEHLSKLSVIRDYKPSNVILNALGOVKMCDGFSIG 201  
 DB 125 VLDKNNITPEDIIGELIAVSIKALEHLSKLSVIRDYKPSNVILNALGOVKMCDGFSIG 184  
 QY 202 YLVDVAKTIDAGCKPYMAPEIRINELNOKGYSKSDIMSGITMELALIRFYPYDSMG 261  
 DB 185 YLVDVAKTIDAGCKPYMAPEIRINELNOKGYSKSDIMSGITMELALIRFYPYDSMG 244  
 QY 262 PFOOLKOVEEPPOLPADKFSAEFVDTSOCLKKNRSEKRPTEPELMQHPEFTLHESKGT 321  
 DB 245 PFOOLKOVEEPPOLPADKFSAEFVDTSOCLKKNRSEKRPTEPELMQHPEFTLHESKGT 304  
 QY 322 DVASFVKLLIGD 333  
 DB 305 DIAAFVAKLLIGD 316

RESULT 3  
 US-10-059-585-36  
 ; Sequence 36, Application US/10059585  
 ; Publication No. US20030082776A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ota, Toshio  
 ; APPLICANT: Isogai, Takao  
 ; APPLICANT: Nishikawa, Tetsuo  
 ; APPLICANT: Hayashi, Koji  
 ; APPLICANT: Otsuka, Kaori  
 ; APPLICANT: Yamamoto, Jun-ichi  
 ; APPLICANT: Ishii, Shizuko  
 ; APPLICANT: Sugiyama, Tomoyasu  
 ; APPLICANT: Wakamatsu, Ai  
 ; APPLICANT: Nagai, Keiichi  
 ; APPLICANT: Otsuki, Tetsuji  
 ; APPLICANT: Funahashi, Shin-ichi  
 ; APPLICANT: Senoo, Chiaki  
 ; APPLICANT: Nezu, Jun-ichi  
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN  
 ; FILE REFERENCE: 06501-098001  
 ; CURRENT FILING DATE: 2002-01-29  
 ; PRIOR APPLICATION NUMBER: PCT/JP00/05060  
 ; PRIOR FILING DATE: 2000-07-28  
 ; PRIOR APPLICATION NUMBER: US 60/183,322  
 ; PRIOR FILING DATE: 2000-02-17  
 ; PRIOR APPLICATION NUMBER: US 60/159,590  
 ; PRIOR FILING DATE: 1999-10-18  
 ; PRIOR APPLICATION NUMBER: JP 2000-118776  
 ; PRIOR FILING DATE: 2000-01-11  
 ; PRIOR APPLICATION NUMBER: JP 2000-183767  
 ; PRIOR FILING DATE: 2000-05-02  
 ; PRIOR APPLICATION NUMBER: JP 11-248036  
 ; PRIOR FILING DATE: 1999-07-29  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SOFTWARE: FastSeq for Windows version 4.0  
 ; SEQ ID NO 36  
 ; LENGTH: 318  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-059-585-36

Query Match 79.0%; Score 1367; DB 9; Length 318;  
 Best Local Similarity 82.7%; Pred. No. 5.4e-114;  
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;

QY 22 POTSSTPRDLDSKACISIGNONFEVKADLEPIEIMELGAGYGVKMRHVPSQIMAVK 81  
 DB 5 PAPNPTPRNDLSRFTITIGDRNEVEADDLVITISLGRGAGYGVKMRHVPSQIMAVK 64  
 QY 82 RIRATVNSQEQKRLMDIDIMRTVDCPTTFYGALFRGADWICMELMDTSLDKFYKQ 141  
 DB 65 RIRATVNSQEQKRLMDIDIMRTVDCPTTFYGALFRGADWICMELMDTSLDKFYKQ 124

QY 22 PQTSTSTPRDLDSKACISISNONFEYKADDELPIMELGSGAYGVEEKMRHVPSCQIMAVK 81  
| : ||||| : | : || : ||||| | ||||| ||||| : || || |||||  
Db 5 PARNPTPRNLDSRFTITIGDRMFEEADLVTTISELGRGAYGVEEKVHAQSGITIMAVK 64

|                       |        |                    |        |             |
|-----------------------|--------|--------------------|--------|-------------|
| Query Match           | 53.1%; | Score 919;         | DB 10; | Length 399; |
| Best Local Similarity | 51.3%; | Pred. No. 6.7e-74; |        |             |

Matches 181; Conservative 56; Mismatches 92; Indels 24; Gaps 6;

QY 1 SOSGKRR-----NGLTIKPE-----AFEOQTSPTPRDDSKACISIG-NQN 44  
 Db 35 SSMGGRKALKLNFPNPFKSTAFITLNPFTGVONPIERLRTHTSISSSKLISPEOH 94  
 QY 45 FEVKADLDLEIMELRGAVGVYVEKRRHVPSSGOIMAVRIRATVNSOEOKRLMDLDISMR 104  
 Db 95 WDTTAEIDLKDLGELGRGAVGVYVKNMVKRPSGOIMAVRIRSTVDEKEKQKOLMDLDVYMR 154  
 QY 105 TVDOPFTVTEYGFALFREGDVAWICMELMDTSLDKFYK--QYIDKQITPEDILGKIVSI 161  
 Db 155 SDDOPYIVQFYGFALFREGDCWICMELMSTSEDKFYKYVSVLD--DVIPPEILGKITAT 212  
 QY 162 VKALEHLSKLVTHRVKPSNNVLINLGOVKMDFGISGLYVDSVATIPAGCKPYMAP 221  
 Db 213 VKALNHLKRNKTIHRDTPSNLILDSNGNKLCDFGISGLVDSIATRDAGCKPYMAP 272  
 QY 222 ERINPELNOKGYSVKSDIWSIGITMIELAILRFPPYDSWGTPEQOLKQVEEPPQLPAD- 280  
 Db 273 ERIDPSASRGQYDVRSDVMSIGITLYELATGRFPYPKMNSVFDQLQYVVKGDPQLSNSE 332  
 QY 281 --KFSAEFVDTSOCLKNKSKERTYPPELMQHPFTTLESKGTDVASFVKIL 331  
 Db 333 EREFSPSFINFVNLCITKDESKRPKYKELKHPIITMYEERAVEVACVCKIL 385

RESULT 6  
 US-09-761-569-6  
 ; Sequence 6, Application US/09761569  
 ; Patent No. US20020102691A1

## GENERAL INFORMATION:

APPLICANT: Davis, Roger J.  
 Raingeaud, Joel  
 Gupta, Shashi  
 Derijard, Benoît  
 TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
 ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
 KINASES

NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/761,569  
 FILING DATE: 16-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/057,009  
 FILING DATE: 1998-04-07

ATTORNEY/AGENT INFORMATION:

NAME: Fasse, J. Peter  
 REGISTRATION NUMBER: 32,983  
 REFERENCE/DOCKET NUMBER: 07917/010001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 363 amino acids  
 TYPE: amino acid

STRANDEDNESS: No. US20020102691A1 Relevant  
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 US-09-761-569-6

Query Match 52.9%; Score 916.5; DB 10; Length 363;  
 Best Local Similarity 54.9%; Pred. No. 9,8e-74;  
 Matches 175; Conservative 53; Mismatches 82; Indels 9; Gaps 4;

QY 20 EOPQTSPTPRDDSKACISIG-NQNFVKADLDLEIMELRGAVGVYVEKRRHVPSSGOIM 78  
 Db 33 QNPHIERLRTHTSISSSKLISPEOHMDTAEIDLKDLGELGRGAVGVYVKNMVKRPSGOIM 92  
 QY 79 AVKRIRATVNSOEOKRLMDLDISMRVDCPTVTEYGFALFREGDVAWICMELMDTSLDKF 138  
 Db 93 AVKRIRSTVDEKEKQKOLMDLDVYVMSDDOPYIVQFYGFALFREGDCWICMELMSTSEDK 152  
 QY 139 YK--QYIDKQITPEDILGKIVSIYKALEHLSKLVTHRVKPSNNVLINLGOVKMDFG 195  
 Db 153 YKYVSVLD--DVIPPEILGKITATYKALNHLKRNKTIHRDTPSNLILDSNGNKLCD 210  
 QY 196 DFGISGLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSDIWSIGITMIELAILRF 255  
 Db 211 DFGISGLVDSIAKTRDAGCKPYMAPERIDPSASRGQYDVRSDVMSIGITLYELATGRFP 270  
 QY 256 YDSWGTPEQOLKQVEEPPQLPAD--KFSAEFVDTSOCLKNKSKERTYPPELMQHPF 312  
 Db 271 YPKMNSVFDQLQYVVKGDPQLSNSEEREFSPSFINFVNLCITKDESKRPKYKELKHPI 330  
 QY 313 FTLESKGTDVASFVKIL 331  
 Db 331 ILMYEERAVEVACVCKIL 349

RESULT 7  
 US-09-761-569-8  
 ; Sequence 8, Application US/09761569  
 ; Patent No. US20020102691A1

## GENERAL INFORMATION:

APPLICANT: Davis, Roger J.  
 Raingeaud, Joel  
 Gupta, Shashi  
 Derijard, Benoît

TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
 ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
 KINASES

NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/761,569  
 FILING DATE: 16-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/057,009  
 FILING DATE: 1998-04-07

ATTORNEY/AGENT INFORMATION:

NAME: Fasse, J. Peter  
 REGISTRATION NUMBER: 32,983  
 REFERENCE/DOCKET NUMBER: 07917/010001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 393 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: No. US20020102691A1 Relevant  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
 US-09-761-569-8

Query Match 52.3%; Score 906; DB 10; Length 393;  
 Best Local Similarity 51.0%; Pred. No. 9.4e-73;  
 Matches 180; Conservative 56; Mismatches 93; Indels 24; Gaps 6;

QY 1 SSGKGRK-----NGLKIPKE-----AFQPOVTSPPRDLDSKACISG-NON 44  
 DB 29 SSMQGRKALKLNPNPFTSTARFTLNPFTGVNPHIERRTHSIESGKLKISPEQH 88  
 QY 45 FEVKADDEPIMELGRAGVVEKMRHVPSCQIMAVKIRATVNSQEQRLMDLDSMR 104  
 DB 89 WDETAEDLKLGEIGRAGVSVNKMVHPSQIMAVKRIRSTVDEKEQRLMDLDSMR 148  
 QY 105 TVDCPTVTFYCALFRGDVWICMELMDTSLDKFYK---QVIDKQOTIPEDILGKIAVSI 161  
 DB 149 SSSCPRTVQFYGALFRGDCDWICMELMSTSPDKFYKYVSVLD--DVIPETILGKITTAT 206  
 QY 162 VVALEHLHSLSVIHRDVKPSNVILNALQYKMGDFGSGYLVDSVAKTIDAGCKPYMAP 221  
 DB 207 VKALMLKENVLKIHRDIKPSNILLDRSGMKIKLDFGSLGVDSIAKTRDAGCRPYMAP 266  
 QY 222 ERINPELNQKGYVKSIVSISLGTIMELAILRFYDSKGTTPQOLKQVVEEPPOLPAD- 280  
 DB 267 ERIDFSASRQGYVRSVWSLIGITLYELATGRFPYKPNVSEFDQLQYVKGDPQLSNSE 326  
 QY 281 --KFSAEVDFETSQLCKKNSKREPTPELMQHPEFTLHESGTDVASFYKIL 331  
 DB 327 EEEFSPSTINFTVNLCLTKDKSKRKYKELLKHPITLMEERAVEACTYCKIL 379

RESULT 8  
 US-10-081-119-20  
 ; Sequence 20, Application US/10081119  
 ; Publication No. US20030045491A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reinhard, Christoph  
 ; APPLICANT: Jefferson, Anne B.  
 ; APPLICANT: Chan, Vivien W.  
 ; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic  
 ; FILE OF INVENTION: Target in Cancer  
 ; FILE REFERENCE: 16932.002  
 ; CURRENT APPLICATION NUMBER: US/10/081.119  
 ; CURRENT FILING DATE: 2002-02-21  
 ; PRIOR APPLICATION NUMBER: 60/289,813  
 ; PRIOR FILING DATE: 2001-02-21  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 20  
 ; LENGTH: 668  
 ; TYPE: PRT  
 ; ORGANISM: Saccharomyces cerevisiae  
 ; US-10-081-119-20

Query Match 35.0%; Score 606; DB 9; Length 668;  
 Best Local Similarity 37.3%; Pred. No. 1.1e-45;  
 Matches 141; Conservative 73; Mismatches 105; Indels 59; Gaps 12;  
 QY 4 GKGRNPGDKT-----PKAEQF-QTSSTPRDLDSK----- 35  
 DB 265 EGRKNPGSLNGVOSTSTSSSTEGPHDYGTTPRGNSSNNSGSGGGGLPANFSKY 324  
 QY 36 ACISIGNNF-----EVKADDEPIMELGRAGVVEKMRHVPSCQ 76  
 DB 325 VDIKSGSLNFAKGLSLSKGIDFNSGSSRHITLDELEFDELGNAGNVSQVLAHPTNV 384  
 QY 77 IMAVRIKATVNSQEQRLMDLDSMRVYVDCPFTVTFYCALFRGDVWICMELMD-TSL 135

DB 365 IMAVEVRLDEANFRQILMELEV-LHKNSBYIYDFYAFLEGAVYKQMEYMDGSL 443  
 QY 136 DFEYKVIDKQOTIPEDILGKIAVSIYKALEHLSKLSVIRDVKPSNVILNA-IGOVKM 194  
 DB 444 KDIYDESEELG-GIDEPOLAFTANAVIHGKELKEQGNIIHRDVKPNILICSAHQYVKL 502  
 QY 195 CDFGSGYLVDSVAKTIDAGCKPYMAPERI--NPELNQKGYSVKSDISLGTIMELAI 251  
 DB 503 CDFGSGYLVDSVAKTIDAGCKPYMAPERI--NPELNQKGYSVKSDISLGTIMELAI 559  
 QY 252 LRFYV--DSWGTTPQOLKQVVEEPPQLADKSAFVDPSTSQLCKKNSKREPTPELMQ 309  
 DB 560 GRYPPEPTIDNIFSLATVDGPPPLPSDKFSDAQDFVSLCLQKIPERRPYAALTE 619  
 QY 310 HPFTLHESKGTVASFY 327  
 DB 620 HPWLKYRNQDVHMSYIL 637

RESULT 9  
 US-09-761-569-13  
 ; Sequence 13, Application US/09761569  
 ; Patent No. US20020102691A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davis, Roger J.  
 ; APPLICANT: Raingeaud, Joel  
 ; APPLICANT: Gupta, Shashi  
 ; APPLICANT: Derijard, Benoit  
 ; TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
 ; ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
 ; KINASES  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/761,569  
 ; FILING DATE: 16-Jan-2001  
 ; CLASSIFICATION: <unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/057,009  
 ; FILING DATE: 1998-04-07  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fasse, J. Peter  
 ; REGISTRATION NUMBER: 32,983  
 ; REFERENCE/DOCKET NUMBER: 07917/010001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617/542-5070  
 ; TELEFAX: 617/542-8906  
 ; TELEX: 200154  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 668 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: No.  
 ; TOPOLOGY: linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 ; US-09-761-569-13

Query Match 35.0%; Score 606; DB 10; Length 668;  
 Best Local Similarity 37.3%; Pred. No. 1.1e-45;  
 Matches 141; Conservative 73; Mismatches 105; Indels 59; Gaps 12;





Verlhard, Benoît  
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND  
ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE  
KINASES

NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/761,569  
 FILING DATE: 16-Jan-2001  
 CLASSIFICATION: <unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/057,009  
 FILING DATE: 1998-04-07  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fasse, J. Peter  
 REGISTRATION NUMBER: 32,983  
 REFERENCE/DOCKET NUMBER: 07917/010001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 400 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: No. US20020102691A1 Relevant  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
 IS-09-761-569-12

```

Query Match      32.7%, Score 566: DB 10, Length 400;
Best Local Similarity 36.5%, Pred. No. 2e+42; 92; Indels 62; Gaps 8;
Matches 125; Conservative 63; Mismatches 92;

QY      32  LDKKACISIGNQNEVKAADLEIPMELTGRGAYGVYKMKRHVPSGQIMAVKRIRATVNSOE 91
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      58  LTKAKVKS-----ELKDDPERISELTGAGNGCVYTKVQHRPSGIMARKLTHTHEIKPAI 111
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      92  QKRLIMDDISKRYVDCPFYTFYFALREGDWTICMELMD-TSLDKFYKQYIDGQITP 150
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      112  RNQIIRLEQV-LHECNSPYIVGFYGAFTSDGETSICMEHMGGSID----QVLKEAKRTP 166
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      151  EDIIKIKAVSIYKALEHLHSKLSYTHRPVKNPENVLIMQVYKMGCDFGISGYLVDSVAKT 210
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      167  EELIKVSTAYVRLGLAYLREKHQIMHRDVKPNILIVNSGEIKLDCDFVSGQILDSIMANS 226
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      211  IDAGCKPYMAPERINPELNQGYSAKSDIWSIGITMIELALLRFPDLS-----WGT 261
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      227  F-VGRSYMAPER---LOGTHYSVOSDIMSGLSLVELAVGGRYPPIPPDAKLEAIFGR 281
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      262  P-----FOOLKQVVEEPSPOLIPADKFSAB 285
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      282  PAVYDEEGEPHSISPPRPPEGRPVSGHMDSRPAAIMFELLDYIVNEPPKLPNGVFTPD 341
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      286  FVDFETSOCLKNSKERPTYPELMOHPFTLLHESGTDVASEV 327
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      342  FOEFVAKCLIKNPAERADLKMLTNHDFIKRSEVEEDFAGWL 383
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
US-09-755-665-34
; Sequence 34, Application US/09755665
; GENERAL INFORMATION:
; PATIENT: Prayaga, Sudhidas K.
; APPLICANT: Majumder, Kumud

```

```

APPLICANT: Tallon, Bruce E.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Macdonnell, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 395
TYPE: PRT
ORGANISM: Homo sapiens
US-09-755-665-34

Query Match          32.5%;   Score 563;   DB 10;   Length 395;
Best Local Similarity 36.9%;   Pred. No. 3,7e+42;
Matches 121;   Conservative 62;   Mismatches 89;   Indels 56;   Gaps 7

```

```

Query Match Similarity      32.5% ; Score 563; DB 10; Length 350;
Best Local Similarity      36.9% ; Pred. No. 3.7e-42;
Matches 121; Conservative 62; Mismatches 89; Indels 56; Gaps 7

QY      EVKADDLPELMELGKAGVYVKEMKHHVPSGQIMAYKRIKATVNSGEOKLMDLDISMRT 105
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      ELKDDDFEELISLGCAGNGGVYTKVQHRPGLIMARKLHLLEIKPAIRNOITELQV-LHE 124
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      106 VCCPFTVYFYGALTFREGDVIWICMELMD-TSLDKFYQVIVDKOTIPEDILGRIVASYKA 164
      | : | | | | : : : | | | | | | | | | | | | | | | | | | | | |
Db      125 CNSPIYVGYGAFYISGELISICMEHDDGSLD---QVLEAKRRIPEELIGKYSIVLARG 180
      | : | | | | : : : | | | | | | | | | | | | | | | | | | | | |

QY      165 LEHLISLKSIVHIRDVKPNSVNLINALQVKKMCDFGISGYLVDSYAKITIDAGCKPYMAPERI 224
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 LAYLRKHQIMHRDVKPNSVNLIVNSRGEIKLCDFGVSGOLIDSMANF-VGTRSYMAPER- 238
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      225 NPELNQKYSVKSADIMSLGITIMLELALIRPPYVS-----WGTP----- 262
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      239 ---LQGTHTSVOSDIMSGLSELVELLVAGRIPIPPPAKELFAIFGRPVYDGEGERPHSIS 295
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      263 -----FOOLKQVVEEPPSPQLPADKFSAEVDFDTSCCLAKNKR 299
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      296 PRRPRPGRPVSGHGMDSRPAMALFEILLDYIVNEPPRLPAGVFTPPDOEYFNKCLIKNPA 355
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      300 ERPTYPELMQHPFTLHESKGTIVASYV 327
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      356 ERADIKMLTNHTFEIKRSEVEEDVFAWGL 383
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Search completed: June 6, 2003, 09:17:20
Job time : 45 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2003, 08:59:23 ; Search time 71 Seconds

(without alignments)  
624.964 Million cell updates/sec

Title: US-09-593-288-2

Perfect score: 1731  
Sequence: 1 SQSGKGRKRNPGIKIPKEAFE.....TLHESKGTDAVFVKLLIGD 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_101002.\*  
1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SID2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SID2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SID2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SID2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID       | Description        |
|------------|-------|-------------|--------|----|----------|--------------------|
| 1          | 1731  | 100.0       | 334    | 18 | AAW19631 | Human mitogen-acti |
| 2          | 1731  | 100.0       | 334    | 18 | AAW06319 | Human mitogen-acti |
| 3          | 1731  | 100.0       | 334    | 20 | AAW97669 | Human mitogen-acti |
| 4          | 1731  | 100.0       | 334    | 21 | AAW57392 | Human MAPK kinase  |
| 5          | 1731  | 100.0       | 334    | 22 | AAW31689 | A human mitogen-ac |
| 6          | 1389  | 80.2        | 267    | 22 | ABG07309 | Novel human diagno |
| 7          | 1384  | 80.0        | 359    | 22 | ABG12149 | Novel human diagno |
| 8          | 1367  | 79.0        | 318    | 18 | AAW06318 | Human mitogen-acti |
| 9          | 1367  | 79.0        | 318    | 20 | AAW97668 | Human mitogen-acti |
| 10         | 1367  | 79.0        | 318    | 22 | AAW31688 | A human mitogen-ac |

|    |       |      |     |    |           |                    |
|----|-------|------|-----|----|-----------|--------------------|
| 11 | 1367  | 79.0 | 318 | 22 | AAW67438  | Amino acid sequenc |
| 12 | 1367  | 79.0 | 318 | 22 | AAW67617  | Amino acid sequenc |
| 13 | 1367  | 79.0 | 318 | 23 | AAW080372 | Human cellular kin |
| 14 | 1295  | 74.8 | 359 | 22 | ABG23442  | Novel human diagno |
| 15 | 1221  | 70.5 | 237 | 23 | ABW57326  | Mouse ischaemic co |
| 16 | 1034  | 59.7 | 334 | 22 | ABW60599  | Drosophila melanog |
| 17 | 920   | 53.1 | 399 | 21 | AAW52302  | Human K309N mutant |
| 18 | 919   | 53.1 | 393 | 18 | AAW06321  | Human mitogen-acti |
| 19 | 919   | 53.1 | 393 | 20 | AAW07671  | Human mitogen-acti |
| 20 | 919   | 53.1 | 393 | 22 | AAW31691  | A human mitogen-ac |
| 21 | 919   | 53.1 | 399 | 18 | AAW06322  | Human mitogen-acti |
| 22 | 919   | 53.1 | 399 | 20 | AAW97672  | Human mitogen-acti |
| 23 | 919   | 53.1 | 399 | 21 | AAW69970  | Human JNK1 protei  |
| 24 | 919   | 53.1 | 399 | 21 | AAW52297  | Human wild-type pr |
| 25 | 919   | 53.1 | 399 | 22 | AAW31692  | A human mitogen-ac |
| 26 | 916.5 | 52.9 | 363 | 18 | AAW06320  | Human mitogen-acti |
| 27 | 916.5 | 52.9 | 363 | 20 | AAW97670  | Human mitogen-acti |
| 28 | 916.5 | 52.9 | 363 | 22 | AAW31690  | A human mitogen-ac |
| 29 | 913   | 52.7 | 399 | 21 | AAW52298  | Human R274G mutant |
| 30 | 912   | 52.7 | 399 | 21 | AAW52300  | Human R274G mutant |
| 31 | 898   | 51.9 | 399 | 21 | AAW20105  | 399-mer protein se |
| 32 | 896   | 51.8 | 399 | 21 | AAW20106  | 399-mer protein se |
| 33 | 892   | 51.5 | 399 | 21 | AAW20107  | 399-mer protein se |
| 34 | 835.5 | 48.3 | 424 | 22 | ABW64620  | Drosophila melanog |
| 35 | 833   | 48.1 | 185 | 22 | AAW72767  | Human, MKK3 protei |
| 36 | 697.5 | 40.3 | 492 | 22 | ABW58135  | Drosophila melanog |
| 37 | 697   | 40.3 | 419 | 20 | AAW22000  | Human MAP kinase k |
| 38 | 697   | 40.3 | 435 | 20 | AAW94849  | Human MAP kinase   |
| 39 | 695   | 40.2 | 419 | 21 | AAW90770  | Human jun N-termin |
| 40 | 694   | 40.1 | 389 | 20 | AAW97663  | Mouse mitogen acti |
| 41 | 694   | 40.1 | 419 | 20 | AAW94851  | Mouse MAPK kinase  |
| 42 | 694   | 40.1 | 419 | 20 | AAW97665  | Mouse mitogen acti |
| 43 | 694   | 40.1 | 468 | 20 | AAW94850  | Mouse MAPK kinase  |
| 44 | 690.5 | 39.9 | 453 | 20 | AAW97667  | Mouse mitogen acti |
| 45 | 687.5 | 39.7 | 333 | 20 | AAW05335  | Human SKK4 protein |

#### ALIGNMENTS

RESULT 1  
AAW19631  
ID AAW19631 standard; Protein; 334 AA.  
AC AAW19631;  
XX 01-SEP-1997 (first entry)  
XX Human mitogen-activated protein kinase MEK6.  
XX MEK-6: mitogen-activated protein kinase kinase; MAPK; p38;  
XX signal transduction; cell proliferation; osteoarthritis; Ischemia;  
XX reperfusion injury; trauma; cancer; autoimmune disease;  
XX rheumatoid arthritis; multiple sclerosis; psoriasis;  
XX inflammatory bowel disease; therapy; diagnosis.  
XX Homo sapiens.  
XX WO9722704-A1.  
XX 26-JUN-1997.  
XX 20-DEC-1996; 96WO-US20233.  
XX 20-DEC-1995; 95US-0576240.  
XX (SIGN-) SIGNAL PHARM INC.  
XX Stein B, Yang MXH;  
XX WPI, 1997-341695/31.  
XX N-PSDB; AAT68716.  
XX

PT Mitogen-activated protein kinase kinase and corresponding DNA -  
 PT phosphorylates p38 cascade members; used in the treatment of  
 PT immunological-related cell proliferative diseases

PS Claim 1: Page 31-33; 67pp; English.

XX Human mitogen-activated protein kinase MEK6 (AAW19631) is a  
 CC protein capable of modulating the activity of the mitogen-activated  
 CC protein kinase p38 (esp. p38-2). Its amino acid sequence was  
 CC deduced from a cDNA clone (AA68716) obtd. from a MOLT-4 cDNA  
 CC library. MEK6 is 88% identical to its closest homologue MKK3,  
 CC and all relevant kinase subdomains are conserved. MEK6  
 CC polypeptides can be produced in transformed or transfected host  
 CC cells. MEK6 and its variants, antibodies raised against MEK6, and  
 CC MEK6 nucleic acids can be used to modulate (stimulate or inhibit)  
 CC phosphorylation of p38 by MEK6 for use in the treatment of diseases  
 CC associated with the p38 cascade e.g. immunological-related cell  
 CC proliferative diseases and autoimmune diseases, and also to detect  
 CC MEK6 kinase activity and identify proteins that interact with MEK6.

XX Sequence 334 AA:

Query Match 100.0%; Score 1731; DB 18; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-163;  
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SOSKGRKRPGLKIPKEAFEPOTSSPPRLDLSKACISIGNONFEVKADDEPIMELGR 60  
 DB 2 SOSKGRKRPGLKIPKEAFEPOTSSPPRLDLSKACISIGNONFEVKADDEPIMELGR 61  
 OY 61 GAYGVEKMRHVPSSQIMAVKRIRATVNSQOKRLMDLDSMRVDCPFTVTFYALFR 120  
 DB 62 GAYGVEKMRHVPSSQIMAVKRIRATVNSQOKRLMDLDSMRVDCPFTVTFYALFR 121  
 OY 121 EGDVWICMELMDTSLDKFYKQVYIDKQGTIPEDILGKIAVSIVKALEHLSKLSVIRHDVK 180  
 DB 122 EGDVWICMELMDTSLDKFYKQVYIDKQGTIPEDILGKIAVSIVKALEHLSKLSVIRHDVK 181  
 OY 181 PSNVLINLGOVKMCDFGISGYLVDSVAKTIDAGCKPYMAPERINPELNQKGSVKSIDIW 240  
 DB 182 PSNVLINLGOVKMCDFGISGYLVDSVAKTIDAGCKPYMAPERINPELNQKGSVKSIDIW 241  
 OY 241 SLGITMIELAILRFPYDSWGTPTFOQLKQVVEEPPSPOLPADKFSAEFVDFTSQCLKNSKE 300  
 DB 242 SLGITMIELAILRFPYDSWGTPTFOQLKQVVEEPPSPOLPADKFSAEFVDFTSQCLKNSKE 301  
 OY 301 RPTYPELMQHPFTLHESKGTDVASFVKILIGD 333  
 DB 302 RPTYPELMQHPFTLHESKGTDVASFVKILIGD 334

RESULT 2

AAW06319 standard; Protein; 334 AA.

XX AAW06319:

XX 07-FEB-1997 (first entry)

DE Human mitogen-activated protein kinase 6.

XX Mitogen-activated protein kinase 6; MKK6; MAP.

XX tyrosine kinase; signal transduction; cytokine; oncoprotein;  
 XX stress; diagnosis; therapy.

XX Homo sapiens.

XX WO9636642-A1.

XX 21-NOV-1996.

XX 26-JAN-1996; 96WO-US01078.

PR 19-SEP-1995; 95US-0530950.  
 PR 19-MAY-1995; 95US-0446083.

XX (DAVI/) DAVIS R J.

XX (DERI/) DERIJARD B.

XX (GUPT/) GUPTA S.

XX (RAIN/) RAINGEAUD J.

XX DAVIS RJ, Derijard B, Gupta S, Raingeaud J;

XX WPI: 1997-012035/01.

XX N-PSDB: AAT43204.

PS Claim 6; Fig 5; 104pp; English.

XX Novel human mitogen activated protein kinase kinase 6 (MKK6)  
 CC (AAW06319) has serine, threonine and tyrosine kinase activity, and  
 CC mediates a signal transduction pathway that activates human  
 CC mitogen-activated protein (MAP) kinase p38. Its amino acid  
 CC sequence was deduced from a cDNA clone (AA43204) obtd. from a human  
 CC skeletal muscle library. Recombinant MKK6 can be produced in  
 CC transformed host cells. MKK6 (AAW06318-22) are useful in the  
 CC treatment of MKK-related disorders, e.g. ischaemic heart disease  
 CC and kidney failure, for identifying modulators of MKK activity,  
 CC and for raising antibodies.

XX Sequence 334 AA:

Query Match 100.0%; Score 1731; DB 18; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-163;  
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SOSKGRKRPGLKIPKEAFEPOTSSPPRLDLSKACISIGNONFEVKADDEPIMELGR 60  
 DB 2 SOSKGRKRPGLKIPKEAFEPOTSSPPRLDLSKACISIGNONFEVKADDEPIMELGR 61  
 OY 61 GAYGVEKMRHVPSSQIMAVKRIRATVNSQOKRLMDLDSMRVDCPFTVTFYALFR 120  
 DB 62 GAYGVEKMRHVPSSQIMAVKRIRATVNSQOKRLMDLDSMRVDCPFTVTFYALFR 121  
 OY 121 EGDVWICMELMDTSLDKFYKQVYIDKQGTIPEDILGKIAVSIVKALEHLSKLSVIRHDVK 180  
 DB 122 EGDVWICMELMDTSLDKFYKQVYIDKQGTIPEDILGKIAVSIVKALEHLSKLSVIRHDVK 181  
 OY 181 PSNVLINLGOVKMCDFGISGYLVDSVAKTIDAGCKPYMAPERINPELNQKGSVKSIDIW 240  
 DB 182 PSNVLINLGOVKMCDFGISGYLVDSVAKTIDAGCKPYMAPERINPELNQKGSVKSIDIW 241  
 OY 241 SLGITMIELAILRFPYDSWGTPTFOQLKQVVEEPPSPOLPADKFSAEFVDFTSQCLKNSKE 300  
 DB 242 SLGITMIELAILRFPYDSWGTPTFOQLKQVVEEPPSPOLPADKFSAEFVDFTSQCLKNSKE 301  
 OY 301 RPTYPELMQHPFTLHESKGTDVASFVKILIGD 333  
 DB 302 RPTYPELMQHPFTLHESKGTDVASFVKILIGD 334

RESULT 3

AAW97669 standard; Protein; 334 AA.

XX AAW97669:

XX 10-MAY-1999 (first entry)

DE Human mitogen activated protein kinase MKK6.

XX MKK6; mitogen activated protein kinase kinase; MAP kinase kinase;  
 XX human; signal transduction; inflammation; psoriasis; AIDS; cancer;

KW apoptosis; therapy.  
 XX Homo sapiens.  
 OS  
 XX MO9902547-A1.  
 XX  
 PD 21-JAN-1999.  
 XX  
 PF 07-JUL-1998; 98WO-US14101.  
 XX  
 PR 07-JUL-1997; 97US-0888429.  
 XX  
 PA (UYMA-) UNIV MASSACHUSETTS.  
 PI Davis RJ, Tourmlier C, Whitmarsh A;  
 XX WPI; 1999-120771/10.  
 DR N-PSDB; AAX07066.  
 XX  
 PT New isolated mitogen-activated protein kinase isoforms - used  
 PT to develop products for treating e.g. inflammatory disorders,  
 XX oxidative damage, proliferative disorders or autoimmune disorders  
 XX  
 PS Disclosure; Page 129; 168pp; English.  
 XX  
 CC This polypeptide comprises human mitogen activated protein (MAP)  
 CC kinase kinase 6 (MKK6). The amino acid sequence was deduced from an  
 CC isolated human skeletal muscle cDNA clone (see AAX07066) and shows  
 CC high homology to human MKK3 (see AAW97668). The human MAP kinase  
 CC kinases MKK3, MKK4, MKK6 and MKK7 (see AAW97664 and AAW97668-72),  
 CC described in the invention, mediate the transduction of specific  
 CC signals from the cell surface to the nucleus along specific  
 CC pathways. They are useful for screening reagents which modulate  
 CC MKK activity. Such agents can be used to prevent or treat  
 CC MKK-mediated disorders, e.g. inflammation, oxidative damage or  
 CC stress-related proliferative disorders, e.g. psoriasis, AIDS,  
 CC malignancies of e.g. the skin, bone marrow, lung, liver, breast,  
 CC gastrointestinal system and genito-urinary tract. Agents which  
 CC inhibit the activity or expression of MKK inhibit cell growth or  
 CC cause apoptosis. MKK7 polynucleotides (see AAX07059-64) and  
 CC polypeptides (see AAW97662-67) are claimed.  
 XX  
 SQ Sequence 334 AA;  
 Query Match 100.0%; Score 1731; DB 20; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-163;  
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SOSKGRKRNPGIKIKREAFEPQSTSTPPRDLDSKACISIGNONFEVKADLEPIIMELGR 60  
 DB 2 SOSKGRKRNPGIKIKREAFEPQSTSTPPRDLDSKACISIGNONFEVKADLEPIIMELGR 61  
 QY 61 GAYGVEKMRHVPSSGQIMAVKRIRATVNSQOKRLMDLDSMRVTDCPTVTFYALFR 120  
 DB 62 GAYGVEKMRHVPSSGQIMAVKRIRATVNSQOKRLMDLDSMRVTDCPTVTFYALFR 121  
 QY 121 EGDVWICMELMDTSLDKFYKQVIDKQGTIPEDILGKIAVSIVKALEHLSKLSVIHRDV 180  
 DB 122 EGDVWICMELMDTSLDKFYKQVIDKQGTIPEDILGKIAVSIVKALEHLSKLSVIHRDV 181  
 QY 181 PSNVLLINALGOVKMCDPFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 240  
 DB 182 PSNVLLINALGOVKMCDPFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 241  
 QY 241 SLGITMIELALIRFPYDSMGTPFOOLKOVVEEPSPOLPADKFSAEFVDFTSQCLKNSKE 300  
 DB 242 SLGITMIELALIRFPYDSMGTPFOOLKOVVEEPSPOLPADKFSAEFVDFTSQCLKNSKE 301  
 QY 301 RPTYPELMQHPFFTLHESKGTDVASFVKILIGD 333  
 DB 302 RPTYPELMQHPFFTLHESKGTDVASFVKILIGD 334

RESULT 4  
 ID AAY57392  
 XX AAY57392 standard; Protein: 334 AA.  
 AC AAY57392;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Human MAPK kinase 6 polypeptide.  
 KW Mitogen-activated protein kinase; MAPK; MAPK kinase 6; antisense;  
 KW sandwich assay; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6033910-A.  
 XX  
 PD 07-MAR-2000.  
 XX  
 PF 19-JUL-1999; 99US-0357073.  
 XX  
 PR 19-JUL-1999; 99US-0357073.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Cowsett LM;  
 XX  
 DR WPI; 2000-269479/23.  
 DR N-PSDB; AAZ98598.  
 XX  
 PT Novel antisense oligonucleotides used for inhibition of  
 PT Mitogen-activated protein kinase kinase 6 expression  
 XX  
 PS Example 13; Columns 45-50; 33pp; English.  
 XX  
 CC The invention provides antisense oligonucleotides which are targeted to a  
 CC nucleic acid encoding a mitogen-activated protein kinase (MAPK) kinase 6.  
 CC The antisense oligonucleotides are used to inhibit MAPK kinase 6  
 CC expression, and so are used to treat diseases mediated by MAPK kinase 6  
 CC expression. They may also be used to detect MAPK kinase 6, e.g. in  
 CC sandwich assays. The present sequence represents the human MAPK kinase 6.  
 XX  
 SQ Sequence 334 AA;  
 Query Match 100.0%; Score 1731; DB 21; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-163;  
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SOSKGRKRNPGIKIKREAFEPQSTSTPPRDLDSKACISIGNONFEVKADLEPIIMELGR 60  
 DB 2 SOSKGRKRNPGIKIKREAFEPQSTSTPPRDLDSKACISIGNONFEVKADLEPIIMELGR 61  
 QY 61 GAYGVEKMRHVPSSGQIMAVKRIRATVNSQOKRLMDLDSMRVTDCPTVTFYALFR 120  
 DB 62 GAYGVEKMRHVPSSGQIMAVKRIRATVNSQOKRLMDLDSMRVTDCPTVTFYALFR 121  
 QY 121 EGDVWICMELMDTSLDKFYKQVIDKQGTIPEDILGKIAVSIVKALEHLSKLSVIHRDV 180  
 DB 122 EGDVWICMELMDTSLDKFYKQVIDKQGTIPEDILGKIAVSIVKALEHLSKLSVIHRDV 181  
 QY 181 PSNVLLINALGOVKMCDPFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 240  
 DB 182 PSNVLLINALGOVKMCDPFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 241  
 QY 241 SLGITMIELALIRFPYDSMGTPFOOLKOVVEEPSPOLPADKFSAEFVDFTSQCLKNSKE 300  
 DB 242 SLGITMIELALIRFPYDSMGTPFOOLKOVVEEPSPOLPADKFSAEFVDFTSQCLKNSKE 301  
 QY 301 RPTYPELMQHPFFTLHESKGTDVASFVKILIGD 333  
 DB 302 RPTYPELMQHPFFTLHESKGTDVASFVKILIGD 334

RESULT 5  
 AAB31689  
 ID AAB31689 standard; Protein: 334 AA.  
 XX  
 AC AAB31689;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE A human mitogen-activated protein kinase MKK6.  
 XX  
 KM Mitogen-activated protein kinase; MAP kinase kinase; MKK; MKK6;  
 KM inflammation; oxidative damage; ischemic heart disease; burn; alcohol;  
 KM kidney failure; liver damage; oxidative stress; rheumatoid arthritis;  
 KM respiratory distress syndrome; septic shock; autoimmune disorder;  
 KM inflammatory disease; proliferative disorder; psoriasis;  
 KM acquired immune deficiency syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6174676-B1.  
 PD 16-JAN-2001.  
 XX  
 PF 08-SEP-1998; 98US-0149879.  
 XX  
 PR 07-APR-1998; 98US-0057009.  
 PR 19-MAY-1995; 95US-0446083.  
 PR 19-SEP-1995; 95US-0530950.  
 XX  
 PA (UYMA-) UNITV MASSACHUSETTS.  
 XX  
 PI Davis RJ, Ralngeaud J, Derlhard B;  
 XX  
 DR WPI: 2001-181551/18.  
 DR N-PSDB; AAF25239.  
 XX  
 PT Identifying mitogen-activating protein kinase activity (MKK), synthesis  
 PT or expression modulators, comprises measuring effect of test reagent on  
 PT MKK phosphorylation, synthesis or expression after incubation with MKK  
 PT  
 XX  
 PS Disclosure: Fig 5A-C; 59pp; English.  
 XX  
 CC The present sequence represents a human mitogen-activated protein (MAP)  
 CC kinase kinase MKK6. The specification describes a method for identifying  
 CC a reagent that modulates mitogen-activating MAP kinase kinase (MKK)  
 CC activity, synthesis or expression. The method comprises incubating MKK  
 CC with the test reagent and measuring the effect of the test reagent on  
 CC phosphorylation, MKK synthesis or MKK expression. MKK modulating reagents  
 CC identified by the method of the invention are useful for treating or  
 CC preventing MKK mediated disorders such as inflammation, oxidative damage,  
 CC ischemic heart disease, burns due to heat or radiation, kidney failure,  
 CC liver damage due to oxidative stress or alcohol, respiratory distress  
 CC syndrome, septic shock, rheumatoid arthritis, autoimmune disorders, and  
 CC other types of inflammatory diseases and stress-related MKK-mediated  
 CC proliferative disorders such as psoriasis, acquired immune deficiency  
 CC syndrome, malignancies of various tissues of the body, including  
 CC malignancies of the skin, bone marrow, lung, liver, breast etc..  
 CC  
 SQ Sequence 334 AA:  
 Query Match 100.0%; Score 1731; DB 22; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 3 Be-163; Indels 0; Gaps 0;  
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SOSGKRRNPGLKIPKEAFEPQPTSTPPRDLDSKACISISIGNONFEVAKADLEPIIMELGR 60  
 DB 2 SOSGKRRNPGLKIPKEAFEPQPTSTPPRDLDSKACISISIGNONFEVAKADLEPIIMELGR 61  
 QY 61 GATGVVKKMRHVPESGQIMAVKRIATVNSQOKRLMDLDLSMKRVDCPTVTFGALFR 120  
 DB 62 GATGVVKKMRHVPESGQIMAVKRIATVNSQOKRLMDLDLSMKRVDCPTVTFGALFR 121

QY 121 EGDWICMELMDTSLDKFPYKQYIDKGORTIPEDILGKIAVSIVKALEHLHSKLSVTHRDYK 180  
 DB 122 EGDWICMELMDTSLDKFPYKQYIDKGORTIPEDILGKIAVSIVKALEHLHSKLSVTHRDYK 181  
 QY 181 PSNVILNAGVKMCDGFIISGYLVDSVAKTIDAGCKPYMAPRINPELNQKGSYKSDIM 240  
 DB 182 PSNVILNAGVKMCDGFIISGYLVDSVAKTIDAGCKPYMAPRINPELNQKGSYKSDIM 241  
 QY 241 SLGITMTELALIRFPYDSWGPFPQOLKQVEEPSQOLPADKPSAEFVDTSCCLKNSKE 300  
 DB 242 SLGITMTELALIRFPYDSWGPFPQOLKQVEEPSQOLPADKPSAEFVDTSCCLKNSKE 301  
 QY 301 RPTYPELMQHPEFTLHESKGTDVASFVKILICD 333  
 DB 302 RPTYPELMQHPEFTLHESKGTDVASFVKILICD 334  
 RESULT 6  
 ABG07309  
 ID ABG07309 standard; Protein: 267 AA.  
 XX  
 AC ABG07309;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #7300.  
 XX  
 KM Human: chromosome mapping; gene mapping; gene therapy; forensic;  
 KM food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US08631.  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HXSFQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI: 2001-639362/73.  
 DR N-PSDB; AAS71496.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity  
 PT  
 XX  
 PS Claim 20; SEQ ID NO 37668; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 267 AA:

Query Match 80.2%; Score 1389; DB 22; Length 267;  
Best Local Similarity 100.0%; Pred. No. 2.5e-129;  
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 67 EKMRRVPSGQIMAVKRRIRATVNSOQKRLMDLDMISMRVDCPTVTFYFGALFRESDVWI 126
DB 1 EKMRRVPSGQIMAVKRRIRATVNSOQKRLMDLDMISMRVDCPTVTFYFGALFRESDVWI 60
QY 127 CMELMDTSLDKFYKYQVIDKGOTIPEDILGKIAVSYKALEHLSKTSYVHRDVKPSNVLI 186
DB 61 CMELMDTSLDKFYKYQVIDKGOTIPEDILGKIAVSYKALEHLSKTSYVHRDVKPSNVLI 120
QY 187 NALGOVKMKDGFISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSKSDIWSLIGITM 246
DB 121 NALGOVKMKDGFISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSKSDIWSLIGITM 180
QY 247 IELAILRPPYDSWGTFFQOLKOVVEPSPOLPADKFSAEFVDFTSOCLKKNKREPTYPE 306
DB 181 IELAILRPPYDSWGTFFQOLKOVVEPSPOLPADKFSAEFVDFTSOCLKKNKREPTYPE 240
QY 307 LMOHPFTLHESKGTDVASFVKLLIGD 333
DB 241 LMOHPFTLHESKGTDVASFVKLLIGD 267

```

#### RESULT 7

```

ID ABG12149 standard; Protein; 359 AA.
XX
AC ABG12149;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #12140.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
DR N-PSDB; AAS76336.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID No 42508; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The

```

polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. Abg00010-Abg30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 359 AA:

Query Match 80.0%; Score 1384; DB 22; Length 359;  
Best Local Similarity 80.2%; Pred. No. 1.2e-128;  
Matches 267; Conservative 33; Mismatches 31; Indels 2; Gaps 2;

```

QY 2 QSKGK-KRNGLKIPKFAFEPOTSSTPRRDLDSKACISIGNONFEVADLEPIMEIGR 60
DB 26 QSKGKSKRRKDLRLSCMS-KPPAPNPPPPRLDSRTFTTIDRNEFEADDLVITSEIGR 84
QY 61 GAYGVVEKMRHVPSGQIMAVKRRIRATVNSOQKRLMDLDMISMRVDCPTVTFYFGALFR 120
DB 85 GAYGVVEKMRHVPSGQIMAVKRRIRATVNSOQKRLMDLDMISMRVDCPTVTFYFGALFR 144
QY 121 EGDVWICMELMDTSLDKFYQVIDKGOTIPEDILGKIAVSYKALEHLSKTSYVHRDVK 180
DB 145 EGDVWICMELMDTSLDKFYQVIDKGOTIPEDILGKIAVSYKALEHLSKTSYVHRDVK 204
QY 181 PSNVLLNALGOVKMKDGFISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSKSDI 240
DB 205 PSNVLLINKBHVCMKDFISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSKSDI 264
QY 241 SLGITMIELAILRPPYDSWGTFFQOLKOVVEPSPOLPADKFSAEFVDFTSOCLKKNKRE 300
DB 265 SLGITMIELAILRPPYDSWGTFFQOLKOVVEPSPOLPADKFSAEFVDFTSOCLKKNKRE 324
QY 301 RPTYPELMOHPFTLHESKGTDVASFVKLLIGD 333
DB 325 RPTYPELMOHPFTLHESKGTDVASFVKLLIGD 357

```

#### RESULT 8

```

ID AAM06318 standard; Protein; 318 AA.
XX
AC AAM06318;
XX
DT 07-FEB-1997 (first entry)
XX
DE Human mitogen-activated protein kinase 3.
XX
KW Mitogen-activated protein kinase 3; MKK3; MAP;
KW tyrosine kinase; signal transduction; cytokine; oncoprotein;
KW stress; diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN WO9636642-A1.
XX
PD 21-NOV-1996.
XX
PR 26-JAN-1996; 96WO-US01078.
XX
PR 19-SEP-1995; 95US-0530950.
PR 19-MAY-1995; 95US-0446083.

```

XX (DAVI/) DAVIS R J.  
 PA (DERI/) DERIJARD B.  
 PA (GUPT/) GUPTA S.  
 PA (RAIN/) RAINGEAUD J.  
 PI Davys RJ, Derijard B, Gupta S, Raingeaud J;  
 DR WPI: 1997-012035/01.  
 DR N-PSDB: AAT43203.  
 PT New mitogen activated protein kinase kinase - useful for treating  
 PT ischemic heart disease, kidney failure etc., also for identifying  
 PT modulators for treatment of similar conditions  
 PS Claim 2; Fig 4; 104pp; English.  
 XX  
 CC Novel human mitogen activated protein kinase kinase 3 (MKK3)  
 CC (AAW06318) has serine, threonine and tyrosine kinase activity, and  
 CC mediates a signal transduction pathway that activates human  
 CC mitogen-activated protein (MAP) kinase p38. Its amino acid  
 CC sequence was deduced from a cDNA clone (AAT43203) cdd. from a human  
 CC foetal brain library. MKK3 is expressed in all tissues tested, but  
 CC partic. in skeletal muscle. Recombinant MKK3 can be produced in  
 CC transformed host cells. MKK3 (AAW06318-22) can be used in the  
 CC treatment of MKK-related disorders, e.g. ischemic heart disease  
 CC and kidney failure, to identify modulators of MKK activity, and  
 CC to raise antibodies.  
 CC  
 SO Sequence 318 AA;  
 Query Match 79.0%; Score 1367; DB 18; Length 318;  
 Best Local Similarity 82.7%; Pred. No. 4,8e-127;  
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;  
 QY 22 POTSSTPPRLDLSKACISIGNONFEVKADLEPIELGKAYGVYVEKRRHVPSCQIMAVK 81  
 DB 5 PAVNPPTPRRLDSRTFTITIGDRNFEVADDLVTISELGRGAYGVYVEKRRHVSQTIMAVK 64  
 QY 82 RIRATVNSOQKRLMDLDSMTVDCPEFTVTFYGFALFRGQDWICHELMDTSLDKFRYKQ 141  
 DB 65 RIRATVNSOQKRLMDLDSMTVDCPEFTVTFYGFALFRGQDWICHELMDTSLDKFRYK 124  
 QY 142 VIDKQTIPEDLIGKIAVSIKALEHLHSLSVIHRDVKPSNVNLINALGOVKMCDPFGISG 201  
 DB 125 VLDKNTIPEDLIGELAVSIKALEHLHSLSVIHRDVKPSNVNLINALGOVKMCDPFGISG 184  
 QY 202 YLVDSVAKTIDAGCKPYMAFERINPELNQGYSVKSDIWSIGITMIELALTRPPYDSMGT 261  
 DB 185 YLVDSVAKTIDAGCKPYMAFERINPELNQGYSVKSDIWSIGITMIELALTRPPYDSMGT 244  
 QY 262 PFOOLKQVVEEPPSPQLPADKESAEFVDFTSQCLKKNKSEKRPYPPELMQHFFTLHESKGT 321  
 DB 245 PFOOLKQVVEEPPSPQLPADKESAEFVDFTSQCLKKNKSEKRPYPPELMQHFFTLHESKGT 304  
 QY 322 DVASEFVKLLIGD 333  
 DB 305 DIAAFVKKILGE 316  
 RESULT 9  
 ID AAW97668 standard; Protein; 318 AA.  
 XX AAW97668;  
 AC  
 DT 10-MAY-1999 (first entry)  
 XX  
 DE Human mitogen activated protein kinase kinase MKK3.  
 XX MKK3; mitogen activated protein kinase kinase; MAP kinase kinase;  
 KW human; signal transduction; inflammation; psoriasis; AIDS; cancer;  
 KW apoptosis; therapy.

XX Homo sapiens.  
 OS  
 PN WO9902547-A1.  
 XX  
 PD 21-JAN-1999.  
 XX  
 PE 07-JUL-1998; 98WO-US14101.  
 XX  
 FR 07-JUL-1997; 97US-0888429.  
 XX  
 PA (UYMA-) UNIV MASSACHUSETTS.  
 PI Davis RJ, Tournier C, Whitmarsh A;  
 DR WPI: 1999-120771/10.  
 DR N-PSDB: AAX07065.  
 XX  
 CC New isolated mitogen-activated protein kinase kinase isoforms - used  
 CC to develop products for treating e.g. inflammatory disorders,  
 CC oxidative damage, proliferative disorders or autoimmune disorders  
 CC  
 CC Example 1; Page 126-127; 168pp; English.  
 CC  
 CC This polypeptide comprises human mitogen activated protein (MAP)  
 CC kinase kinase 3 (MKK3), a 36 kDa protein that phosphorylates p38 but  
 CC not JNK1 or ERK2. The amino acid sequence was deduced from an  
 CC isolated human brain cDNA clone (see AAX07065). The human MAP kinase  
 CC kinases MKK3, MKK4, MKK6 and MKK7 (see AAW97664 and AAW97668-72),  
 CC described in the invention, mediate the transduction of specific  
 CC signals from the cell surface to the nucleus along specific  
 CC pathways. They are useful for screening reagents which modulate  
 CC MKK activity. Such agents can be used to prevent or treat  
 CC stress-related disorders, e.g. inflammation, oxidative damage or  
 CC malignancies of e.g. the skin, bone marrow, lung, liver, breast,  
 CC gastrointestinal system and genito-urinary tract. Agents which  
 CC inhibit the activity or expression of MKK inhibit cell growth or  
 CC cause apoptosis. MKK7 polynucleotides (see AAX07059-64) and  
 CC polypeptides (see AAW97662-67) are claimed.  
 CC  
 SO Sequence 318 AA;  
 Query Match 79.0%; Score 1367; DB 20; Length 318;  
 Best Local Similarity 82.7%; Pred. No. 4,8e-127;  
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;  
 QY 22 POTSSTPPRLDLSKACISIGNONFEVKADLEPIELGKAYGVYVEKRRHVPSCQIMAVK 81  
 DB 5 PAVNPPTPRRLDSRTFTITIGDRNFEVADDLVTISELGRGAYGVYVEKRRHVSQTIMAVK 64  
 QY 82 RIRATVNSOQKRLMDLDSMTVDCPEFTVTFYGFALFRGQDWICHELMDTSLDKFRYKQ 141  
 DB 65 RIRATVNSOQKRLMDLDSMTVDCPEFTVTFYGFALFRGQDWICHELMDTSLDKFRYK 124  
 QY 142 VIDKQTIPEDLIGKIAVSIKALEHLHSLSVIHRDVKPSNVNLINALGOVKMCDPFGISG 201  
 DB 125 VLDKNTIPEDLIGELAVSIKALEHLHSLSVIHRDVKPSNVNLINALGOVKMCDPFGISG 184  
 QY 202 YLVDSVAKTIDAGCKPYMAFERINPELNQGYSVKSDIWSIGITMIELALTRPPYDSMGT 261  
 DB 185 YLVDSVAKTIDAGCKPYMAFERINPELNQGYSVKSDIWSIGITMIELALTRPPYDSMGT 244  
 QY 262 PFOOLKQVVEEPPSPQLPADKESAEFVDFTSQCLKKNKSEKRPYPPELMQHFFTLHESKGT 321  
 DB 245 PFOOLKQVVEEPPSPQLPADKESAEFVDFTSQCLKKNKSEKRPYPPELMQHFFTLHESKGT 304  
 QY 322 DVASEFVKLLIGD 333  
 DB 305 DIAAFVKKILGE 316  
 RESULT 10



AAB31688  
 ID AAB31688 standard; Protein; 318 AA.  
 AC AAB31688;  
 XX  
 XX  
 XX 30-APR-2001 (first entry)  
 DE A human mitogen-activated protein kinase MKK3.  
 XX  
 XX Mitogen-activated protein kinase; MAP kinase kinase; MKK; MKK3;  
 KW inflammation; oxidative damage; ischemic heart disease; burn; alcohol;  
 KW kidney failure; liver damage; oxidative stress; rheumatoid arthritis;  
 KW respiratory distress syndrome; septic shock; autoimmune disorder;  
 KW inflammatory disease; proliferative disorder; psoriasis;  
 KW acquired immune deficiency syndrome.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX US6174676-B1.  
 PN 16-JAN-2001.  
 PD  
 XX  
 XX 08-SEP-1998; 98US-0149879.  
 PF  
 XX 07-APR-1998; 98US-0057009.  
 PR 19-MAY-1995; 95US-0446083.  
 PR 19-SEP-1995; 95US-0530950.  
 XX  
 XX (UYMA-) UNIV MASSACHUSETTS.  
 PA  
 XX  
 XX Davis RJ, Raingeaud J, Derjard B;  
 PI WPI; 2001-181551/18.  
 DR N-PSDB; AAF25238.  
 DR  
 XX  
 XX Identifying mitogen-activating protein kinase activity (MKK), synthesis  
 PT or expression modulators, comprises measuring effect of test reagent on  
 PT MKK phosphorylation, synthesis or expression after incubation with MKK  
 PT  
 XX  
 XX Example 1; Fig 4; 59pp; English.  
 XX  
 XX The present sequence represents a human mitogen-activated protein (MAP)  
 CC kinase kinase MKK3. The specification describes a method for identifying  
 CC a reagent that modulates mitogen-activating MAP kinase kinase (MKK)  
 CC activity, synthesis or expression. The method comprises incubating MKK  
 CC with the test reagent and measuring the effect of the test reagent on  
 CC phosphorylation, MKK synthesis or MKK expression. MKK modulating reagents  
 CC identified by the method of the invention are useful for treating or  
 CC preventing MKK mediated disorders such as inflammation, oxidative damage,  
 CC ischemic heart disease, burns due to heat or radiation, kidney failure,  
 CC liver damage due to oxidative stress or alcohol, respiratory distress  
 CC syndrome, septic shock, rheumatoid arthritis, autoimmune disorders, and  
 CC other types of inflammatory diseases and stress-related MKK-mediated  
 CC proliferative disorders such as psoriasis, acquired immune deficiency  
 CC syndrome, malignancies of various tissues of the body, including  
 CC malignancies of the skin, bone marrow, lung, liver, breast etc..  
 XX  
 XX  
 SQ Sequence 318 AA;  
 Query Match 79.0%; Score 1367; DB 22; Length 318;  
 Best Local Similarity 82.7%; Pred. No. 4.8e-127;  
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;  
 OY 22 POTSPPDDLSKACISIGNONFEVKADDEPIMELGRGAYGVVERHVPSSQIMAVK 81  
 DB 5 PAVNPPTPPRNLDISGTTIGDRNFEVADDLVTISELGRGAYGVVERHVPSSQIMAVK 64  
 OY RIRATVNSQEQKRLMDLISMRTVDCPTVTFYGLFRGDWICMELMDTSIDKRYKQ 141  
 DB 65 RIRATVNSQEQKRLMDLISMRTVDCPTVTFYGLFRGDWICMELMDTSIDKRYK 124  
 OY 142 VIDKQOTIPEDILGIAVSIKALEHLSKLSVTHRDVPSVNLINALGQVKKMCDGFIGS 201

DB 125 VLKNNMTIPEDILGIAVSIKALEHLSKLSVTHRDVPSVNLINALGQVKKMCDGFIGS 184  
 OY 202 YLVDVAKTIDAGCKPYAPERINDELNKGYSVDISGITMTEALILRPYDSKGT 261  
 DB 185 YLVDVAKTIDAGCKPYAPERINDELNKGYSVDISGITMTEALILRPYDSKGT 244  
 OY 262 PFQOLKQVEEPPSPQLPADKFSAEFVDFTSQCLKNSKRPYPELMOHPFTLHESKGT 321  
 DB 245 PFQOLKQVEEPPSPQLPADKFSAEFVDFTSQCLKNSKRPYPELMOHPFTLHESKGT 304  
 OY 322 DVASEFVKILTD 333  
 DB 305 DIAAFVKILGE 316

RESULT 11  
 AAG67438  
 ID AAG67438 standard; Protein; 318 AA.  
 AC AAG67438;  
 XX  
 XX  
 XX 26-NOV-2001 (first entry)  
 DE Amino acid sequence of a human polypeptide.  
 XX  
 XX Human; protein kinase; protein phosphatase; signal transduction;  
 KW intracellular signalling pathway.  
 KW  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200109345-A1.  
 PN 08-FEB-2001.  
 PD  
 XX  
 XX 28-JUL-2000; 2000WO-JP05060.  
 PF  
 XX 29-JUL-1999; 99JP-0248036.  
 PR 18-OCT-1999; 99US-0159590.  
 PR 11-JAN-2000; 2000JP-0118776.  
 PR 17-FEB-2000; 2000US-0183322.  
 PR 02-MAY-2000; 2000JP-0183767.  
 XX  
 XX (HELI-) HELIX RES INST.  
 PA  
 XX  
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;  
 PI Senoo C, Nezu J;  
 XX WPI; 2001-564736/63.  
 DR  
 XX  
 XX New genes encoding protein kinase and protein phosphatase, useful for  
 PT identifying modulators which can be used to treat human or animal  
 PT disorders associated with the expression or function of these enzymes -  
 XX  
 XX Example 4; Page 207-210; 336pp; Japanese.  
 XX  
 XX The specification describes human protein kinase/protein phosphatases.  
 CC The polypeptides are expected to participate in signal transduction  
 CC in cells. The kinase phosphatases are connected with intracellular  
 CC signalling pathways. Antisense oligonucleotides and compounds  
 CC identified by screening (agonists or antagonists) can be used to  
 CC treat human or animal disorders associated with the expression  
 CC or function of the protein. In addition, the polypeptides may be used  
 CC as target molecules for drug development. The present sequence  
 CC represents a polypeptide, used in the course of the invention.  
 XX  
 XX  
 SQ Sequence 318 AA;  
 Query Match 79.0%; Score 1367; DB 22; Length 318;  
 Best Local Similarity 82.7%; Pred. No. 4.8e-127;  
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;



CC related diseases. The method of the invention comprises contacting a  
 CC test compound with at least one of the cellular kinases RICK, RIK,  
 CC NCK-interacting kinase, MKK3 and SRPK-2 and detecting any change in  
 CC kinase activity. The method of the invention can be used to treat and/or  
 CC prevent CMV infections and related diseases. Oligonucleotides that can  
 CC detect the specified kinases can also be used for diagnosis of infection.  
 CC The present amino acid sequence represents the human cellular kinase MKK3  
 CC protein of the invention, as described above.

XX Sequence 318 AA;

Query Match 79.0%; Score 1367; DB 23; Length 318;  
 Best Local Similarity 82.7%; Pred. No. 4,8e-127;  
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;

QY 22 POTSPPRDLDSKACISIGNONFEVKADLLEPIMELGAGVYKRMHVPSCQIMAYK 81  
 Db 5 PAPNTPPRNDSKRFITIGDRNFEVADLVITISLGGAVGVKVRHQAOSGTLMAVK 64  
 QY 82 RIRATVNSQEQKRLMDLIDISMRVDCPTVTYFGALFREGDWMICMELMDTSLDKFKYK 141  
 Db 65 RIRATVNSQEQKRLMDLIDINMRVDCPTVTYFGALFREGDWMICMELMDTSLDKFKYK 124  
 QY 142 VIDGQRTPEIDILCKIAVSIYKALEHHSKLSVIRDVYKPSVNLINALGQVKMCDFGISG 201  
 Db 125 VLDKNNITPEIDILGIAVSIYKALEHHSKLSVIRDVYKPSVNLINKEGHVKMCDFGISG 184  
 QY 202 YLVDSVAKTIDAGCKPYMAPERINPELNOKGYSKSDIWSLGITMIELALPEPDSMGT 261  
 Db 185 YLVDSVAKTMDAGCKPYMAPERINPELNOKGYNKSDVWSLGITMIELALPEPDSMGT 244  
 QY 262 PFOOLKQVEPSPQOLPADKFSAEFVDFTSOCLKNKSERPTYPELMOHPFTLHESKGT 321  
 Db 245 PFOOLKQVEPSPQOLPADRSPFEVDFTAOCLRNKPAERMSYLELMEHPFTLHKTCT 304  
 QY 322 DVASFVKLIIGD 333  
 Db 305 DIAAFVKLIIGE 316

RESULT 14

ID ABG23442 standard; Protein; 359 AA.

AC ABG23442;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #23433.

KW Human: chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PE 30-MAR-2001; 2001WO-0508631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSF-) HYSFQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

XX N-PSDB; AAS87629.

PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity

PS Claim 20; SEQ ID No 53801; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 359 AA;

Query Match 74.8%; Score 1295; DB 22; Length 359;  
 Best Local Similarity 76.0%; Pred. No. 8.1e-120;  
 Matches 253; Conservative 35; Mismatches 43; Indels 2; Gaps 2;

QY 2 QSKGK-KRNGCLKIPKAEFOPOTSPPRDLDSKACISIGNONFEVKADLLEPIMEGR 60  
 Db 26 QSKGKSKRRKDLRISCMS-KPAPNTPPRNDSKRFITIGDRNFEVADLVITISLGR 84  
 QY 61 GAYGVYKRMHVPSCQIMAYKRIATVNSQEQKRLMDLIDISMRVDCPTVTYFGALFR 120  
 Db 85 GAYGVYKVRHQAOSGTLMAVKRIATVNSQEQKRLMDLIDINMRVDCPTVTYFGALFR 144  
 QY 121 EGDVWICMELMDTSLDKFKYKQVIDKGQITPEIDILGIAVSIYKALEHHSKLSVIRDVYK 180  
 Db 145 EGDVWICMELMDTSLDKFKYKVDKNNITPEIDILGIAVSIYKALEHHSKLSVIRDVYK 204  
 QY 181 PSNVNLINALGQVYKMCDFGISGYLVDSYAKTIDAGCKPYMAPERINPELNOKGYSKSDI 240  
 Db 205 PSNVNLINKEGHVKMCDFGISGYLVDSYAKTIDAGCKYKHGHSLEPNLNRKGCYKSHW 264  
 QY 241 SIGITMIELALPEPDSMGTPOOLKQVVEPSPQOLPADKFSAEFVDFTSOCLKNKSK 300  
 Db 265 SIGITMIELALPEPDSMGTPOOLKQVVEPSPQOLPADRSPFEVDFTAOCLRNKPAE 324  
 QY 301 RPTYPELMOHPFTLHESKGTDAFVKLIIGD 333  
 Db 325 RMSYLELMEHPFTLHKTETDIAAFVKLIIGE 357

RESULT 15

ID ABB57326 standard; Protein; 237 AA.

AC ABB57326;

DE 07-MAR-2002 (first entry)

DE Mouse ischemic condition related protein sequence SEQ ID NO:907.

KW Mouse; ischemia; compressive ischemia; occlusive ischemia;

KW vasospastic ischemia; ischemic condition; ischemic disease.

OS Mus musculus.

Fri Jun 6 15:36:17 2003

us-09-593-288-2.rag

Page 10

PN W0200188188-A2.

PD 22-NOV-2001.

PF 18-MAY-2001; 2001WO-JP04192.

PR 18-MAY-2000; 2000JP-0145977.

PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON

PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

DR WPI; 2002-034733/04.

DR N-PSDB; ABI99801.

Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes -

PS Claim 2; Page 2293-2294; 2690pp; English.

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring the expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in AB857020 to AB857374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.

| Sequence | 237 AA |
|----------|--------|
| sq       |        |

| Query match | Score | DB  | Length |
|-------------|-------|-----|--------|
| 70.58;      | 1221; | 23; | 237;   |

|         |      |              |    |            |    |        |    |      |    |
|---------|------|--------------|----|------------|----|--------|----|------|----|
| Matches | 231; | Conservative | 3; | Mismatches | 3; | Indels | 0; | Gaps | 0; |
|---------|------|--------------|----|------------|----|--------|----|------|----|

|         |      |              |    |            |    |        |    |      |    |
|---------|------|--------------|----|------------|----|--------|----|------|----|
| Matches | 231; | Conservative | 3; | Mismatches | 3; | Indels | 0; | Gaps | 0; |
|---------|------|--------------|----|------------|----|--------|----|------|----|

97 MDLISMRTVDCPETVIEYGALFREGBWICMELMDISLDNF INQ IDABQIIFEDIGN 100

Db 1 MDLDSMRIVDCPFIIVIEYGALEKEGDVWICMEIMDISDNE INQV IDNQG I IFEDJON 00

15/ JAVSLVKALEHLHSKLSV I HKDVNFSNVLINLSVQVNMCDI GIGGIDVDOVMN1JDNCON 22

DB 61 LAWSI VKALEHLSALSY INKDVAFSN EINI DQY V KKKDZ OJDOZ LIDZYV... ..

ZI/ PIMAFERINPELUNGISVANDIMSDGINTENTENK ADOCHOL XXENG X

QY

DB 121 PIMAF ENIN EUNQNOI DVNDD INOJOT IITDEBETEN A BODICORR K KKKK

Z / EFADNF SAE VDE I00CEINNOENEA Y A CAG... : ...

101. LEADERSHIP AND THE ORGANIZATION OF THE WORKING CLASS

Search completed: June 6, 2003, 09:10:29  
Job time : 73 secs

Job time : 73 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2003, 09:07:33 ; Search time 19 Seconds

(without alignments)  
1684.882 Million cell updates/sec

Title: US-09-593-288-2

Perfect score: 1731

Sequence: 1 SOSGKRRNPGLKIPKEAFE.....TLHESKGTDAVFKLLGD 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------|-------------|
| 1          | 1731  | 100.0   | 334          | 2     | S71631      |
| 2          | 1705  | 98.5    | 334          | 2     | S71632      |
| 3          | 1367  | 79.0    | 318          | 2     | A55556      |
| 4          | 924.5 | 53.4    | 445          | 2     | S36039      |
| 5          | 922.5 | 53.3    | 457          | 2     | A54694      |
| 6          | 919   | 53.1    | 399          | 2     | I38901      |
| 7          | 882   | 51.0    | 395          | 2     | S52423      |
| 8          | 865.5 | 50.0    | 345          | 2     | T16665      |
| 9          | 822   | 47.5    | 162          | 2     | S71633      |
| 10         | 628.5 | 36.3    | 363          | 2     | T22107      |
| 11         | 618   | 35.7    | 359          | 2     | T26025      |
| 12         | 610.5 | 35.3    | 505          | 2     | T16583      |
| 13         | 607.5 | 35.1    | 605          | 2     | S18648      |
| 14         | 606   | 35.0    | 668          | 2     | S56909      |
| 15         | 587   | 33.9    | 393          | 1     | A45100      |
| 16         | 587   | 33.9    | 393          | 1     | JN0840      |
| 17         | 586.5 | 33.9    | 393          | 1     | I59571      |
| 18         | 586.5 | 33.9    | 401          | 1     | I52829      |
| 19         | 586   | 33.9    | 393          | 1     | A42068      |
| 20         | 583   | 33.7    | 400          | 1     | A48081      |
| 21         | 575   | 33.2    | 395          | 1     | S36186      |
| 22         | 572   | 33.0    | 393          | 1     | S46361      |
| 23         | 565   | 32.6    | 397          | 1     | S41054      |
| 24         | 563   | 32.5    | 400          | 1     | A46723      |
| 25         | 560   | 32.4    | 1218         | 2     | T29915      |
| 26         | 552   | 31.9    | 444          | 2     | A56708      |
| 27         | 541   | 31.3    | 393          | 1     | A45176      |
| 28         | 525   | 30.3    | 387          | 1     | A56466      |
| 29         | 508.5 | 29.4    | 435          | 2     | T37324      |

## ALIGNMENTS

|    |       |      |     |   |        |                    |
|----|-------|------|-----|---|--------|--------------------|
| 30 | 502.5 | 29.0 | 355 | 2 | T02056 | protein kinase MEK |
| 31 | 487   | 28.1 | 448 | 2 | T16256 | hypothetical prote |
| 32 | 486   | 28.1 | 357 | 2 | T06583 | protein kinase MEK |
| 33 | 482.5 | 27.9 | 363 | 2 | T51992 | MAP kinase kinase  |
| 34 | 481   | 27.8 | 515 | 2 | A25048 | regulatory protein |
| 35 | 478.5 | 27.6 | 363 | 2 | T51294 | MAP kinase kinase  |
| 36 | 476.5 | 27.5 | 508 | 2 | A48069 | MAP kinase kinase  |
| 37 | 473   | 27.3 | 363 | 2 | T08542 | mitogen-activated  |
| 38 | 472   | 27.3 | 363 | 2 | T51735 | mitogen-activated  |
| 39 | 469   | 27.1 | 354 | 2 | T04262 | mitogen-activated  |
| 40 | 460.5 | 26.6 | 518 | 2 | S53804 | mitogen-activated  |
| 41 | 456.5 | 26.4 | 340 | 1 | OKBRT1 | protein kinase NPK |
| 42 | 448.5 | 25.9 | 306 | 2 | S69045 | protein kinase byr |
| 43 | 434.5 | 25.1 | 520 | 2 | T51338 | protein kinase MKK |
| 44 | 395.5 | 22.8 | 449 | 2 | T16259 | mitogen-activated  |
| 45 | 363.5 | 21.0 | 310 | 2 | G96761 | hypothetical prote |
|    |       |      |     |   |        | probable MAP kinas |

## RESULT 1

S71631  
mitogen-activated protein kinase kinase (EC 2.7.1.-) 6 [similarity] - human

N:Alternate names: MAP kinase kinase SAPK3

C:Species: Homo sapiens (man)

C>Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 08-Sep-2000

C:Accession: S71631; A59347

R:Cuenda, A.; Alonso, G.; Morrice, N.; Jones, M.; Meier, R.; Cohen, P.; Nebreda, A.

A>Title: Purification and cDNA cloning of SAPK3, the major activator of RK/p38 in

A:Reference number: S71631; MUID:97015116; PMID:8861944

A:Accession: S71631

A:Molecule type: mRNA

A:Residues: 1-334 <CDS>

A:Cross-references: EMBL:X96757; NID:G1495484; PIDN:CA65532.1; PID:G1495485

A:Experimental source: cell type B cell; cell line BUB

J.Han, J.; Lee, J.D.; Jiang, Y.; Li, Z.; Feng, L.; Ulevitch, R.J.

A:Title: Characterization of the structure and function of a novel MAP kinase kinas

A:Reference number: A59347; MUID:96216353; PMID:8621675

A:Accession: A59347

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 57-124, 'M', 126-334 <HAN>

A:Cross-references: GB:039064; NID:G1209670; PIDN:AAB03708.1; PID:G1209671

C:Gene: GDB:MAP2K6; PRKMK6; MEK6; MKK6; SAPK3

A:Cross-references: GDB:1230470; OMIM:601254

C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: Arp; phosphotransferase

F:51-314/Domain: protein kinase homology <KIN>

F:59-67/Region: protein kinase ATP-binding motif

Query Match 100.0%; Score 1731; DB 2; Length 334;

Best Local Similarity 100.0%; Pred. No. 1, 5e-82;

Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | SOSGKRRNPGLKIPKEAFEQPTSSPPRDLDSKACISIGNQNEVKAADLEPMEIGR       | 60  |
| DB | 2   | SOSGKRRNPGLKIPKEAFEQPTSSPPRDLDSKACISIGNQNEVKAADLEPMEIGR       | 61  |
| QY | 61  | GAYGVKRMHVPESGQIMAYKRIATVNSOQKRLMDLDSMKRYVDCPFYVTFGALFR       | 120 |
| DB | 62  | GAYGVKRMHVPESGQIMAYKRIATVNSOQKRLMDLDSMKRYVDCPFYVTFGALFR       | 121 |
| QY | 121 | EGDVWICMELMDTSIDKFKYQVVDKQTIPEDIIGKIAVSIVKALEHLSKLSYTHRYVK    | 180 |
| DB | 122 | EGDVWICMELMDTSIDKFKYQVVDKQTIPEDIIGKIAVSIVKALEHLSKLSYTHRYVK    | 181 |
| QY | 181 | PSNVLTINALGVKMKCPGSGISGYLVDAKTIIDAGCKRYMAPERINPELNQKGYSVKSDIW | 240 |
| DB | 182 | PSNVLTINALGVKMKCPGSGISGYLVDAKTIIDAGCKRYMAPERINPELNQKGYSVKSDIW | 241 |

QY 241 SLGITMIELALIRFPYDSWGTSPFOQLKQVVEEPPSPOLPADKFSAEFVDTSOCLKNSKE 300  
 DB 242 SLGITMIELALIRFPYDSWGTSPFOQLKQVVEEPPSPOLPADKFSAEFVDTSOCLKNSKE 301  
 QY 301 RPTYPELMOHPEFTLHESKGTDAVAFYKLLIGD 333  
 DB 302 RPTYPELMOHPEFTLHESKGTDAVAFYKLLIGD 334

## RESULT 2

MAP kinase kinase (EC 2.7.1.-) SAPK3 isoform A - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 20-Jun-2000  
 C:Accession: S71632  
 R:Cluend, A.; Alonso, G.; Morrice, N.; Jones, M.; Meller, R.; Cohen, P.; Nebreda, A.R.  
 EMBO J. 15, 4156-4164, 1996  
 A:Title: Purification and cDNA cloning of SAPK3, the major activator of RK/p38 in stress  
 A:Reference number: S71631; MUID:97015116; PMID:8661944  
 A:Accession: S71632  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-334 <CDS>  
 A:Cross-references: EMBL:X97052; NID:q1495701; PIDN:CAA65764.1; PID:q1495702  
 A:Experimental source: cell type fibroblast  
 C:Genetics:  
 A:Gene: SAPK3  
 C:Superfamily: kinase-related transforming protein; protein kinase homology  
 C:Keywords: ATP; phosphotransferase  
 F:51-314/Domain: protein kinase homology <KIN>  
 F:59-67/Region: protein kinase ATP-binding motif

Query Match 98.5%; Score 1705; DB 2; Length 334;  
 Best Local Similarity 97.9%; Pred. No. 3,3e-81;  
 Matches 326; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 SOSGKRRNGIKIPEAFEPQTSPPEDLSKACISIGNQFEVKADLEPIMELGR 60  
 DB 2 SOSGKRRNGIKIPEAFEPQTSPPEDLSKACISIGNQFEVKADLEPIMELGR 61  
 QY 61 GAYGVKKRHHVPSGOIMAVKIRATVNSQQRLLMDLDSMTYVDCPTVTFYCALFR 120  
 DB 62 GAYGVKKRHHVPSGOIMAVKIRATVNSQQRLLMDLDSMTYVDCPTVTFYCALFR 121  
 QY 121 EGDVWICMELMTSLDKFKYQVINDKQOTIPEDILGKIAVSIVKALEHLHSLKSLVYHFDVK 180  
 DB 122 EGDVWICMELMTSLDKFKYQVINDKQOTIPEDILGKIAVSIVKALEHLHSLKSLVYHFDVK 181  
 QY 181 PSNVLINALGVKMCDFGISIGYLVDSYAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 240  
 DB 182 PSNVLINALGVKMCDFGISIGYLVDSYAKTIDAGCKPYMAPERINPELNOKGYSVKSDIW 241  
 QY 241 SLGITMIELALIRFPYDSWGTSPFOQLKQVVEEPPSPOLPADKFSAEFVDTSOCLKNSKE 300  
 DB 242 SLGITMIELALIRFPYDSWGTSPFOQLKQVVEEPPSPOLPADKFSAEFVDTSOCLKNSKE 301  
 QY 301 RPTYPELMOHPEFTLHESKGTDAVAFYKLLIGD 333  
 DB 302 RPTYPELMOHPEFTLHESKGTDAVAFYKLLIGD 334

## RESULT 3

MAP kinase kinase (EC 2.7.1.-) 3 [similarity] - human  
 A:Accession: A55556  
 N:Alternate names: MAP kinase kinase 3 (MKK3)  
 C:Species: Homo sapiens (man)  
 C>Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 08-Sep-2000  
 C:Accession: A55556  
 R:Berlhard, B.; Ringeaud, J.; Barrett, T.; Wu, I.H.; Han, J.; Ulevitch, R.J.; Davis, R.  
 Science 267, 682-685, 1995  
 A:Title: Independent human MAP kinase signal transduction pathways defined by MEK and MK  
 A:Reference number: A55556; MUID:95141073; PMID:7839144

A:Accession: A55556  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-318 <EB>  
 A:Cross-references: GB:L36719; NID:q685173; PIDN:AAC41718.1; PID:q685174  
 C:Genetics:  
 A:Gene: GDB:MAP2K3; PRKMK3; MEK3; MKK3  
 A:Cross-references: GDB:9539640; OMIM:602315  
 A:Map position: 17q11.2-17q11.2  
 C:Superfamily: kinase-related transforming protein; protein kinase homology  
 C:Keywords: ATP; phosphotransferase  
 F:33-296/Domain: protein kinase homology <KIN>  
 F:41-49/Region: protein kinase ATP-binding motif

Query Match 79.0%; Score 1367; DB 2; Length 318;  
 Best Local Similarity 82.7%; Pred. No. 7,8e-64;  
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;

QY 22 POTSPPRDLDSKACISIGNQFEVKADLEPIMELGRGAYGVKKRHHVPSGOIMAVK 81  
 DB 5 PARNPPRRMIDSNRTFTTIDRNEVEADLVITSEIGRGAYGVKKRHHVPSGOIMAVK 64  
 QY 82 RIRATVNSQQRLLMDLDSMTYVDCPTVTFYCALFRGDAVWICMELMTSLDKFKYK 141  
 DB 65 RIRATVNSQQRLLMDLDSMTYVDCPTVTFYCALFRGDAVWICMELMTSLDKFKYK 124  
 QY 142 VIDKQOTIPEDILGKIAVSIVKALEHLHSLKSLVYHFDVKPSNVLINALGVKMCDFGISG 201  
 DB 125 VLDRKMTIPEDILGKIAVSIVKALEHLHSLKSLVYHFDVKPSNVLINALGVKMCDFGISG 184  
 QY 202 YLVDVSAKTMAGCKPYMAPERINPELNOKGYSVKSDIWSLGITMIELALIRFPYDSWGT 261  
 DB 185 YLVDVSAKTMAGCKPYMAPERINPELNOKGYSVKSDIWSLGITMIELALIRFPYDSWGT 244  
 QY 262 PFOQLKQVVEEPPSPOLPADKFSAEFVDTSOCLKNSKEPRPTYPELMOHPEFTLHESGT 321  
 DB 245 PFOQLKQVVEEPPSPOLPADKFSAEFVDTSOCLKNSKEPRPTYPELMOHPEFTLHESGT 304  
 QY 322 DVASFYKLLIGD 333  
 DB 305 DIAAFYKLLIGD 316

## RESULT 4

MAP kinase activator 2 - African clawed frog (fragment)  
 C:Species: Xenopus laevis (African clawed frog)  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 19-Dec-1997  
 C:Accession: S36039  
 R:Yashear, B.M.  
 Submitted to the EMBL Data Library, May 1993.  
 A:Reference number: S36039  
 A:Accession: S36039  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-445 <YAS>  
 A:Cross-references: EMBL:222736  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase  
 F:146-413/Domain: protein kinase homology <KIN>  
 F:154-162/Region: protein kinase ATP-binding motif

Query Match 53.4%; Score 924.5; DB 2; Length 445;  
 Best Local Similarity 53.4%; Pred. No. 6,3e-41;  
 Matches 183; Conservative 51; Mismatches 92; Indels 17; Gaps 5;

QY 1 SOSGKRRNGIKIPEAFEPQTSPPEDLSKACISIGNQFEVKADLEPIMELGR 52  
 DB 94 SYOKQDLRHSKALSTNEQATKRLERLTHS-----ISSGKRLSPQHDWDFYADL 148  
 QY 53 EPIMEIGRGAYGVKKRHHVPSGOIMAVKIRATVNSQQRLLMDLDSMTYVDCPTV 112  
 DB 149 KDLGETGRGAYGVKKRHHVPSGOIMAVKIRATVNSQQRLLMDLDSMTYVDCPTV 208

666T-UNU-OT agnirg\_7vay4 OCT 09 08 00 AM EST

PF000000000: protein kinase homology <KIN>



F:106-114/Region: protein kinase ATP-binding motif

Query Match 51.0%; Score 882; DB 2; Length 395;  
Best Local Similarity 51.0%; Pred. No. 8,6e-39;  
Matches 180; Conservative 60; Mismatches 87; Indels 26; Gaps 9;

QY 1 SSKGKKR-----NGKIPKFAFEPQSSSTP-----PDDLSKACISIG-  
DB 33 SSMGKKRRRLKLNFPNPPKSTARRFTNPTTGVONPHIERLRHSISGKLIKSPKCH  
QY 45 FEVKAADLEPIEMELGRGAVGVYKRRHVPSCQIMAVKRIRATVNSQEQKRLMDISMR  
DB 93 WDFPAEDKIDGELGRGAVGVYKRRHVPSCQIMAVKRIRATVNSQEQKRLMDISMR  
QY 105 TVDCPTVTFYFALFREGDVMICELMDISLDRK---QVIDKQITPEDILGKIVSI  
DB 153 SSQCPYIYQFYGALFREGDVMICELMDISLDRK---DIVPEELIGITLAT  
QY 162 VKALEHLHSKSVIHRDVKPSNVILNALGVKMGDFGIGYLVDSVAKTIDAGCKRYMAP  
DB 211 VKALNHL-KLEIHRDVKPSNVILNALGVKMGDFGIGYLVDSVAKTIDAGCKRYMAP  
QY 222 ERINPELNQGVYKRRHVPSCQIMAVKRIRATVNSQEQKRLMDISMR  
DB 270 ERIDPSNRQGVYKRRHVPSCQIMAVKRIRATVNSQEQKRLMDISMR  
QY 281 KFSF-EFVDTSQCLAKNKRPPYPELMOHPEFLHESKGTVDASFEVKLLI  
DB 329 ERSSPPSPFINFNLCTIKRDESKRPYKELKHPFLIMYERIEVACVCKIL

# RESULT 8

T16655  
hypothetical protein R0365.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 18-Feb-2000  
C:Accession: T16655  
R:Connell, M.  
Submitted to the EMBL Data Library, March 1996  
A:Description: The sequence of C. elegans cosmid R0365.  
A:Reference number: 218556  
A:Accession: T16655  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-343 <CON>  
A:Cross-references: EMBL:U51994; NID:q1255290; PID:q1255295; PIDN:AAA96067.1; GSPDB:GN00  
A:Experimental source: strain Bristol N2; clone R0365  
A:Gene: CESP:R0365.2  
A:Map position: X  
A:Introns: 5/1: 35/2: 79/3: 207/3: 291/2  
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 50.0%; Score 865.5; DB 2; Length 343;  
Best Local Similarity 50.8%; Pred. No. 5.3e-38;  
Matches 168; Conservative 64; Mismatches 88; Indels 11; Gaps 6;

QY 2 OSKGRKR--PGLKIPKFAFEPQSSSTP-----PDDLSKACISIG-  
DB 2 ERKGRERKLPKMT-----VMPFVPEPTNMLDRCLIKLTNESEELIATDLVLEEL  
QY 59 GRGAVGVYKRRHVPSCQIMAVKRIRATVNSQEQKRLMDISMRVYDCEFTYFYGAL  
DB 57 GRGAVGVYKRRHVPSCQIMAVKRIRATVNSQEQKRLMDISMRVYDCEFTYFYGAL  
QY 119 FRGCDVMICELMDISLDRK---QVIDKQITPEDILGKIVSI  
DB 117 FRGCDVMICELMDISLDRK---QVIDKQITPEDILGKIVSI  
QY 179 VKRSNVLINLGVKMGDFGIGYLVDSVAKTIDAGCKRYMAPERINPELNQGVYKSD  
DB 177 VKRSNVLINLGVKMGDFGIGYLVDSVAKTIDAGCKRYMAPERINPELNQGVYKSD

QY 239 INSLGTTMELALNRPYDSWGTPEQOLQOVVEPSPQLPADK-FSNEFYDTSCCLKN  
DB 236 VMSLGTITLIEAVGTGPRVANKKPPFQOLQOVVEPSPQLPADK-FSNEFYDTSCCLKN  
QY 298 SKERPYPELMOHPEFLHESKGTVDASFEVKLLI  
DB 296 YNERPKYPPELLAMPFMEQARNEKQFSNARFI

# RESULT 9

S71633  
MAP kinase kinase (EC 2.7.1.-) SAPK3 isoform B - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 20-Jun-2000  
C:Accession: S71633  
R:Quenda, A.; Alonso, G.; Morrice, N.; Jones, M.; Meier, R.; Cohen, P.; Nebreda, A.R.  
EMBO J 15, 4156-4164, 1996  
A:Title: Purification and cDNA cloning of SAPK3, the major activator of Rb/p38 in s  
A:Reference number: S71631; MUID:97015116; PMID:8661944  
A:Accession: S71633  
A:Molecule type: mRNA  
A:Residues: 1-162 <CUE>  
A:Cross-references: EMBL:X98067; NID:q1495709; PIDN:CAA66670.1; PID:q1495710  
A:Experimental source: cell type fibroblast  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1996  
A:Note: only a part of the nucleic acid sequence is shown; only a part of the transl  
C:Genetics:  
A:Gene: SAPK3b  
C:Superfamily: kinase-related transforming protein; protein kinase homology  
C:Keywords: ATP; phosphotransferase  
F:1-162/Domain: protein kinase homology (fragment) <KIN>

Query Match 47.5%; Score 822; DB 2; Length 162;  
Best Local Similarity 98.1%; Pred. No. 4.6e-36;  
Matches 159; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 69 MRHVPSCQIMAVKRIRATVNSQEQKRLMDISMRVYDCEFTYFYGALFREGDVMIC  
DB 1 MRHVPSCQIMAVKRIRATVNSQEQKRLMDISMRVYDCEFTYFYGALFREGDVMIC  
QY 129 ELMDISLDRK---QVIDKQITPEDILGKIVSIKALEHLHSKSVIHRDVKPSNVILNA  
DB 61 ELMDISLDRK---QVIDKQITPEDILGKIVSIKALEHLHSKSVIHRDVKPSNVILNA  
QY 189 LGQVYKMGDFGIGYLVDSVAKTIDAGCKRYMAPERINPELNQ  
DB 121 LGQVYKMGDFGIGYLVDSVAKTIDAGCKRYMAPERINPELNQ

# RESULT 10

T22107  
hypothetical protein F42G10.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T22107; T26026  
R:Harris, B.  
Submitted to the EMBL Data Library, February 1995  
A:Reference number: Z19515  
A:Accession: T22107  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-363 <MID>  
A:Cross-references: EMBL:Z48230; PIDN:CAA88264.1; GSPDB:GN00028; CESP:F42G10.2  
A:Experimental source: clone F42G10  
R:Leonard, N.  
Submitted to the EMBL Data Library, May 1997  
A:Reference number: Z20139  
A:Accession: T26026  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-363 <MID>  
A:Cross-references: EMBL:Z48230; PIDN:CAA88264.1; GSPDB:GN00028; CESP:F42G10.2  
A:Experimental source: clone VZC374L



## C:Genetics:

A:Gene: CESP:F42G10.2

A:Map position: X

A:Introns: 42/2; 95/3; 136/3; 176/3; 236/3; 259/3; 281/3; 310/2; 332/2

C:Superfamily: kinase-related transforming protein; protein kinase homology

## Query Match

Best Local Similarity 36.3%; Score 628.5; DB 2; Length 363;

Matches 136; Conservative 56; Mismatches 111; Indels 39; Gaps 7;

QY 21 QPQSSSTPRDLSDKACISIGNQ-----FEVAKADLEPIIM 56  
 Db 16 PPSLSSTPRSLSYN-----GNEKLPEESVLRSLSTGLKYPDDEHLITFSSANLQDQ 70  
 QY 57 ELGRGAGVVEKMHVPSGQIMAVKRIIA-TVNSGEORLMDLDSMRVTCPTVTFT 115  
 Db 71 AIGNGNGVYKMKHKEGKILIAVKRIKNNIGHEQJRLREHDTYKSEKGPNIYKRY 130  
 QY 116 GALEFREGDVMICELMDTSLDKFYKOV-IDKQGTIPEDILGKIAIVKALEHLSKLSV 174  
 Db 131 GALEFSEGDVMICELMDISMDLTKRYVMKNSRLNENYGHITTCYDADLYLKKELKI 190  
 QY 175 IHRDVKPSNVLINAGVKKMDGISTGYVDSVAKTIDACKKPYAPRINDELNOKGS 234  
 Db 191 IHRDVKPSNVLINAGVKKMDGISTGYVDSVAKTIDACKKPYAPRINDELNOKGS 247  
 QY 235 VKSDIMSLGITMELALIRFPYDSMGTPFOOLKQVVEEPPQLPADK---FSAFVDF 290  
 Db 248 VRSDVMSLGITLVEIATGKFPYQEMNSLFQDIATVSSDPRILHPSDFHSLPLVAFI 307  
 QY 291 SOCLTKKSKRPYVPELMQHPFTLHESKGTDVASFVKLLIG 332  
 Db 308 NCLTKDRHRPRYDTLKSFPYKIVAVAGPEIEE-AKRILG 348

## RESULT 11

T26025

hypothetical protein VZC374L.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C&gt;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000

C:Accession: T26025

R:Lenard, N.

submitted to the EMBL Data Library, May 1997

A:Reference number: Z20139

A:Accession: T26025

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-359 &lt;WILD&gt;

A:Cross-references: EMBL:Z59122; PIDD:CA08354.1; GSPDB:GN00028; CESP:VZC374L.1

A:Experimental source: clone VZC374L

C:Genetics:

A:Gene: CESP:VZC374L.1

A:Map position: X

A:Introns: 40/2; 93/3; 132/3; 172/3; 232/3; 255/3; 277/3; 306/2; 328/2

C:Superfamily: kinase-related transforming protein; protein kinase homology

## Query Match

Best Local Similarity 45.6%; Score 618; DB 2; Length 359;

Matches 131; Conservative 47; Mismatches 99; Indels 10; Gaps 5;

QY 51 DLEPIMELGAGVVEKMHVPSGQIMAVKRIIRATVNSGEORLMDLDSMRVTCPT 110  
 Db 63 NLRHLSOYAGAGYGVHMKQHNHESGLIAVKRIIRATVNSGEORLMDLDSMRVTCPT 121  
 QY 111 TYTEFGALFREGDVMICELMDTSLDKFYKOV-IDKQGTIPEDILGKIAIVKALEHLS 169  
 Db 122 IYKFGAGFSEGDVMICELMDISMDLTKRYVMKNSRLNENYGHITTCYDADLYLKKELKI 190  
 QY 170 SKLSYIHRDVKPSNVLINAGVKKMDGISTGYVDSVAKTIDACKKPYAPRINDELN 229  
 Db 182 RKLNIHRDVKPSNVLINAGVKKMDGISTGYVDSVAKTIDACKKPYAPRINDELN 238  
 QY 230 QKGSYVKSIDIMSLGITMELALIRFPYDSMGTPFOOLKQVVEEPPQLPADKSAFVDF 288

Db 239 MDXYDIRSDVMSLGITLVEIATGKFPYQEMNSLFQDIATVSSDPRILHPSDFHSLPLVAFI 298  
 QY 289 ---FTSOLKSKSKRPYVPELMQHPFTLHESKGTDVASFVKLLIG 332  
 Db 299 LCRFINCLKRNKDRPRYVNLKTFSPYKIVAVAGPEIEE-AKRILG 344

## RESULT 12

T16583

hypothetical protein K08A8.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C&gt;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C:Accession: T16583

R:Pauley, A.

submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid K08A8.

A:Reference number: Z18541

A:Accession: T16583

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-505 &lt;PAU&gt;

A:Cross-references: EMBL:U038377; NID:G1022966; PID:G1022969; PIDN:AAA79746.1; CESP

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:K08A8.1

A:Introns: 62/1; 139/3; 187/3; 291/3; 345/2; 380/2; 448/3

## Query Match

Best Local Similarity 35.3%; Score 610.5; DB 2; Length 505;

Matches 131; Conservative 63; Mismatches 116; Indels 21; Gaps 7;

QY 13 KIPKEAFQDQSTPRDLSDKACISIGNQ-----EVRAD--DLEPIMELGAGA 62  
 Db 26 QMPQAPRHPHPSRS---NDHNVMKLMKQAEENGUYTLQGNRRKADKEIQVYEDIGHG 82  
 QY 63 YGVVEKMRHVPSSGQIMAVKRIIRATVNSGEORLMDLDSMRVTCPTVTFTYFALREG 122  
 Db 83 CGTVYKCR--KSVIMAVVMTPTNSYSESRILMDVCLSPDCYIYRCGYFTTNF 140  
 QY 123 DWIMCELMDSLDKRYKOVIDKQGTIPEDILGKIAIVKALEHLSKLSVIRVYKPS 182  
 Db 141 DVAVCECMATCIDLRL--LIRIKQPIPERIEIKLSVITKALHYLTKHQIHNRVYKPS 197  
 QY 183 NYLINAGVKKMDGISTGYVDSVAKTIDACKKPYAPRINDELNOKGSYVKSIDIMSL 242  
 Db 198 NLLDMSGVYKILCDGFIAGRLIESRAHSKQAGCPLVMGPRIIDPN-NFDSYDIRDVMSF 256  
 QY 243 GITMELALIRFPYDSMGTPFOOLKQVVEEPPQLPADKSAFVDFTSOLKSKSKRP 302  
 Db 257 GVTLEIATGKFPYQEMNSLFQDIATVSSDPRILHPSDFHSLPLVAFI 314  
 QY 303 TYPMLQHPFTLHESKGTDVASFVKLLIGD 333  
 Db 315 NYDMLQHPFVAVHHEKIETDVEWFAVDVGD 345

## RESULT 13

S18648

protein kinase w1sl (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C&gt;Date: 22-Nov-1993 #sequence\_revision 10-Feb-1995 #text\_change 10-Dec-1999

C:Accession: S18648; T40435

R:Marbrick, E.; Panties, P.A.

EMBO J. 10, 4291-4299, 1991

A:Title: The w1sl protein kinase is a dosage-dependent regulator of mitosis in schi

A:Reference number: S18648; MUID:92097549; PMID:1756736

A:Accession: S18648

A:Molecule type: DNA

A:Residues: 1-605 &lt;WAB&gt;

A:Cross-references: EMBL:X62631; NID:G5141; PIDN:CAA44499.1; PID:G5142

R:Lyne, M.H.; Rajandream, M.A.; Barrell, B.G.; Chillingworth, T.; Churcher, C.M.

submitted to the EMBL Data Library, August 1999



R;Zheng, C.F.; Guan, K.L.  
 J. Biol. Chem. 268, 11435-11439, 1993  
 A;Title: Cloning and characterization of two distinct human extracellular signal-regulated  
 A;Reference number: A46723; MUID:93266604; PMID:8388392  
 A;Accession: B46723  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-295, 'G', 296-393 <ZHE>  
 A;Cross-references: GB:L11284; NID:g307183  
 A;Note: sequence extracted from NCBI backbone (NCBI:P:132852)  
 R;Mansour, S.J.; Reising, K.A.; Candi, J.M.; Hermann, A.S.; Gloor, J.W.; Herskind, K.R.;  
 J. Biochem. 116, 304-314, 1994  
 A;Title: Mitogen-activated protein (MAP) kinase phosphorylation of MAP kinase kinase: De  
 A;Reference number: JC2504; MUID:95122457; PMID:7822248  
 A;Accession: JC2504  
 A;Molecule type: protein  
 A;Residues: 5-96;98-349;354-393 <MAN>  
 A;Note: phosphorylation sites determined in vitro  
 C;Comment: This enzyme is activated by protein kinase raf-1 (see PIR:A00637). It in turn  
 C;Genetics:  
 A;Gene: GDB:PRKMK1; MEK1; MAPKK1  
 A;Cross-references: GDB:136418; OMIM:176872  
 C;Complex: monomer  
 C;Function:  
 A;Description: catalyzes the formation of specific peptidyl-threonine-phosphate and pept  
 A;Pathway: MAP kinase cascade  
 C;Superfamily: kinase-related transforming protein; protein kinase homology  
 C;Keywords: alternative splicing; ATP; monomer; phosphoprotein; phosphotransferase; ser1  
 F:1-393/Product: MAP kinase kinase 1, splice form A #status experimental <MATA>  
 F:1-146,173-393/Product: MAP kinase kinase 1, splice form B #status predicted <MATB>  
 F:66-361/Domain: protein kinase ATP-binding motif  
 F:74-82/Region: protein kinase homology  
 F:97,114,190,192/Active site: Lys, Glu, Asp, Lys #status predicted  
 F:218,222/Binding site: phosphate (Ser) (covalent) (by raf-1 kinase) #status predicted  
 F:292,386/Binding site: phosphate (Thr) (covalent) (by raf-1 kinase) #status experimental

Query Match 33.9%; Score 587; DB 1; Length 393;  
 Best Local Similarity 38.0%; Pred. No. 1.3e-23;  
 Matches 125; Conservative 62; Mismatches 90; Indels 52; Gaps 7;

QY 46 EVKADLEPIMELGAGVVEKMRHVPSSGOTAVKRIATVNSQEQRLMDLDSMRT 105  
 DB 62 ELKDDDFEKISLGLGNGGVKRVSHKPSGLVMARKLIHLKPAIRMQIIRLOV-LHE 120  
 QY 106 VDCPTVTYFYGALFREGDVMICMLMD-TSLDKFYQVIDKGOTIPEDITIGKIVASIVKA 164  
 DB 121 CNSPYIVGFYGFYSDGEISICMEHMDGSLD---QVLKAGRIPEQIIIGKIVAYIKG 176  
 QY 165 LEHLHSKLSVIRHDKPNSVNLINALGVKMCDPGISGYLVDSVAKTIDAGCKPYMAPERI 224  
 DB 177 LTVLEKHKIMHRDVKPSNIIIVNSRGEIKLCDPFGVSGQLIDSMANSF-VGTRSYNSPER- 234  
 QY 225 NPELNOKGYSVKSDIMSLGITMIELAILRFPY-----DSMGTP----- 262  
 DB 235 ---LQGTIVSYQSDIWSMGLSIVENAVGRYPIPPDAKLELMFGCQVEGDAETPPRPR 291  
 QY 263 -----PQQLKQVVEPSPQLPADKPSAEFVFTSCLKNSKERPT 303  
 DB 292 TPGRPILSSYGMDSRPPMAIFELDIYVNEPPKLPSPGVSTLEFQDFVNNKCLIKNPAERAD 351  
 QY 304 YPELMOHPFTLHESKGTDVASVFKLIIG 332  
 DB 352 LKQLMVHAFIKRSDEAEVDFAGWLCSTIG 380

Search completed: June 6, 2003, 09:11:51  
 Job time : 21 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2003, 09:04:09 ; Search time 11 Seconds

(without alignments)  
1255.602 Million cell updates/sec

Title: US-09-593-288-2

Perfect score: 1731  
Sequence: 1 SOSKGRKRNGLKIPKEAF.....TLHESKGTDAVFAFKLLIGD 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID         | Description         |
|------------|-------|-------------|--------|------------|---------------------|
| 1          | 1731  | 100.0       | 334    | MPK6_HUMAN | P52564 homo sapien  |
| 2          | 1705  | 98.5        | 334    | MPK6_MOUSE | P70236 mus musculu  |
| 3          | 1367  | 79.0        | 318    | MPK3_HUMAN | P46734 homo sapien  |
| 4          | 1334  | 77.1        | 314    | MPK3_MOUSE | O09110 mus musculu  |
| 5          | 924.5 | 53.4        | 446    | MPK2_XENLA | Q07192 xenopus lae  |
| 6          | 920   | 53.1        | 397    | MPK4_MOUSE | P47809 m dual spec  |
| 7          | 919   | 53.1        | 399    | MPK4_HUMAN | P55985 homo sapien  |
| 8          | 697   | 40.3        | 419    | MPK7_HUMAN | O14733 homo sapien  |
| 9          | 696   | 40.2        | 487    | HEP_DROME  | Q23977 drosophila   |
| 10         | 628.5 | 36.3        | 363    | YR62_CAEEL | Q20347 caenorhabdi  |
| 11         | 607.5 | 35.1        | 605    | WIS1_SCHPO | P33886 schizosacch  |
| 12         | 606   | 35.0        | 668    | PBS2_YEAST | F08018 saccharomyc  |
| 13         | 587.5 | 33.9        | 448    | MPK5_YEAST | O62862 rattus norv  |
| 14         | 587   | 33.9        | 392    | MPK1_HUMAN | O02750 homo sapien  |
| 15         | 587   | 33.9        | 392    | MPK1_MOUSE | P31938 mus musculu  |
| 16         | 587   | 33.9        | 392    | MPK1_RAT   | O01966 mus musculu  |
| 17         | 586.5 | 33.9        | 401    | MPK2_MOUSE | O63932 mus musculu  |
| 18         | 586   | 33.9        | 392    | MPK1_RABIT | P29678 oryctolagus  |
| 19         | 584   | 33.7        | 388    | MPK1_SERCA | O91447 serinus can  |
| 20         | 583   | 33.7        | 400    | MPK2_RAT   | P36506 rattus norv  |
| 21         | 575   | 33.2        | 394    | MPK1_XENLA | O05116 xenopus lae  |
| 22         | 572   | 33.0        | 393    | MPK1_CRIGR | O63960 cricetus     |
| 23         | 571   | 33.0        | 398    | MPK2_CHICK | O90891 gallus galli |
| 24         | 565   | 32.6        | 397    | MPK2_CYPCA | O90321 cyprinus ca  |
| 25         | 563   | 32.5        | 400    | MPK2_HUMAN | P36507 homo sapien  |
| 26         | 553   | 31.9        | 438    | MPK5_HUMAN | O13163 homo sapien  |
| 27         | 541   | 31.3        | 393    | DSOR_DROME | O24324 drosophila   |
| 28         | 525   | 30.3        | 387    | MEK2_CAEEL | O10664 caenorhabdi  |
| 29         | 490.5 | 28.3        | 435    | MEK2_MOUSE | O99078 ussilaago ma |
| 30         | 481   | 27.8        | 515    | STF7_YEAST | P06784 saccharomyc  |
| 31         | 478.5 | 27.6        | 363    | SKH1_SCHPO | O9y884 schizosacch  |
| 32         | 476.5 | 27.5        | 508    | MKR1_YEAST | P32490 saccharomyc  |
| 33         | 456.5 | 26.4        | 340    | BYR1_SCHPO | P10506 schizosacch  |

|    |       |      |     |   |            |                    |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 448.5 | 25.9 | 506 | 1 | MKK2_YEAST | P32491 saccharomyc |
| 35 | 418.5 | 24.2 | 491 | 1 | STK3_HUMAN | O13188 homo sapien |
| 36 | 418   | 24.1 | 487 | 1 | STK4_HUMAN | O13043 homo sapien |
| 37 | 368.5 | 21.3 | 968 | 1 | ST10_HUMAN | O4804 homo sapien  |
| 38 | 364.5 | 21.1 | 966 | 1 | ST10_MOUSE | O55098 mus musculu |
| 39 | 350   | 20.2 | 589 | 1 | STF7_CANAL | P46599 candida alb |
| 40 | 335   | 19.4 | 426 | 1 | ST25_HUMAN | O00506 homo sapien |
| 41 | 332.5 | 19.2 | 443 | 1 | ST24_HUMAN | O9y6e0 homo sapien |
| 42 | 330   | 19.1 | 426 | 1 | ST25_MOUSE | O9y2w1 mus musculu |
| 43 | 316.5 | 18.3 | 658 | 1 | PAK1_SCHPO | P50527 schizosacch |
| 44 | 315   | 18.2 | 544 | 1 | PAK3_RAT   | O62829 rattus norv |
| 45 | 312.5 | 18.1 | 393 | 1 | NTF4_TORAC | O40532 nicotiana t |

## ALIGNMENTS

| RESULT 1 | ID   | MPK6_HUMAN | STANDARD; | PRT; | 334 AA. |
|----------|--|------------|-----------|------|---------|
| AC       | P52564;  |            |           |      |         |
| DT       | 01-OCT-1996 (Rel. 34, Created)   |            |           |      |         |
| DT       | 01-OCT-1996 (Rel. 34, Last sequence update)                            |            |           |      |         |
| DT       | 15-JUN-2002 (Rel. 41, Last annotation update)                          |            |           |      |         |
| DE       | Dual specificity mitogen-activated protein kinase 6                    |            |           |      |         |
| DE       | (EC 2.7.1.-) (MAP kinase kinase 6) (MAPK 6) (MAPK/ERK kinase 6)        |            |           |      |         |
| DE       | (SAPK3).   |            |           |      |         |
| GN       | MAP2K6 OR PRKMK6 OR MKK6 OR MEK6.                                      |            |           |      |         |
| OS       | Homo sapiens (Human).  |            |           |      |         |
| OC       | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;                |            |           |      |         |
| OC       | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.              |            |           |      |         |
| OX       | NCBI_TaxID:9606;   |            |           |      |         |
| RN       | [1]  |            |           |      |         |
| RP       | SEQUENCE FROM N.A., AND MUTAGENESIS.                                   |            |           |      |         |
| RC       | TISSUE=Skeletal muscle;  |            |           |      |         |
| RA       | MEDLINE=96182129; PubMed=8622669;                                      |            |           |      |         |
| RT       | Raingeaud J., Whitmarsh A.J., Barrett T., Derjard B., Davis R.J.;      |            |           |      |         |
| RT       | "MKK3- and MKK6-regulated gene expression is mediated by the p38       |            |           |      |         |
| RT       | mitogen-activated protein kinase signal transduction pathway.";        |            |           |      |         |
| RL       | Mol. Cell. Biol. 16:1247-1255(1996).                                   |            |           |      |         |
| RN       | [2]  |            |           |      |         |
| RP       | SEQUENCE FROM N.A.   |            |           |      |         |
| RC       | TISSUE=T-cell;   |            |           |      |         |
| RA       | MEDLINE=96212215; PubMed=8626699;                                      |            |           |      |         |
| RT       | Stein B., Brady H., Yang M.X., Young D.B., Barbosa M.S.;               |            |           |      |         |
| RT       | "Cloning and characterization of MEK6, a novel member of the mitogen-  |            |           |      |         |
| RT       | activated protein kinase cascade.";                                    |            |           |      |         |
| RL       | J. Biol. Chem. 271:11427-11433(1996).                                  |            |           |      |         |
| RN       | [3]  |            |           |      |         |
| RP       | SEQUENCE FROM N.A., AND MUTAGENESIS (SHORT FORM).                      |            |           |      |         |
| RC       | TISSUE=Placenta;   |            |           |      |         |
| RA       | MEDLINE=96216153; PubMed=8621675;                                      |            |           |      |         |
| RT       | Han J., Lee J.-D., Jiang Y., Li Z., Feng L., Ulevitch R.J.;            |            |           |      |         |
| RT       | "Characterization of the structure and function of a novel MAP kinase  |            |           |      |         |
| RL       | kinase (MKK6).";   |            |           |      |         |
| RL       | J. Biol. Chem. 271:2886-2891(1996).                                    |            |           |      |         |
| RN       | [4]  |            |           |      |         |
| RP       | SEQUENCE FROM N.A.   |            |           |      |         |
| RA       | MEDLINE=96278799; PubMed=8663074;                                      |            |           |      |         |
| RT       | Moriguchi T., Kuroyanagi N., Yamaguchi K., Gotoh Y., Irie K., Kano T., |            |           |      |         |
| RT       | Shitaraabe K., Muro Y., Shibuya H., Matsumoto K., Nishida E.,          |            |           |      |         |
| RT       | Hagiwara M.;   |            |           |      |         |
| RT       | "A novel kinase cascade mediated by mitogen-activated protein kinase   |            |           |      |         |
| RL       | kinase 6 and MKK3.";   |            |           |      |         |
| RL       | J. Biol. Chem. 271:13675-13679(1996).                                  |            |           |      |         |
| RN       | [5]  |            |           |      |         |
| RP       | SEQUENCE FROM N.A.   |            |           |      |         |
| RA       | MEDLINE=97015116; PubMed=8861944;                                      |            |           |      |         |
| RT       | Cebeda A., Alonso G., Morrice N., Jones M., Meier R., Cohen P.,        |            |           |      |         |
| RT       | Nebreda A.R.;  |            |           |      |         |
| RT       | "Purification and cDNA cloning of SAPK3, the major activator of        |            |           |      |         |
| RT       | RK/p38 in stress- and cytokine-stimulated monocytes and epithelial     |            |           |      |         |
| RT       | cells.";   |            |           |      |         |

EMBO J. 15:4156-4164(1996).

[6]

CLEAVAGE BY ANTHRAX LETHAL FACTOR.

MEDLINE-20558083; PubMed-11104681;

RA Vitale G., Bernardi L., Napolitani G., Mock M., Montecucco C.;

RT "Susceptibility of mitogen-activated protein kinase family

RL members to proteolysis by anthrax lethal factor."

Biochem. J. 352:739-745(2000).

CC -1- FUNCTION: CATALYZES THE CONCOMITANT PHOSPHORYLATION OF A THREONINE

CC AND A TYROSINE RESIDUE IN MAP KINASE P38 EXCLUSIVELY.

CC -1- ENZYME REGULATION: PROBABLY ACTIVATED BY DUAL PHOSPHORYLATION ON

CC SER-207 AND THR-211.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: MKK6 AND MKK6B (SHOWN HERE); ARE

CC PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: MKK6 IS ONLY EXPRESSED IN SKELETAL MUSCLE.

CC MKK6B, ON THE OTHER HAND, IS FOUND IN SKELETAL MUSCLE, HEART, AND

CC IN LESSEER EXTENT IN LIVER OR PANCREAS.

CC -1- INDUCTION: STRONGLY ACTIVATED BY UV, ANISOMYCIN, AND OSMOTIC SHOCK

CC BUT NOT BY PHORBOL ESTERS, NGF OR EGF.

CC -1- PRT: VERY LOW AUTOPHOSPHORYLATION.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC MAP KINASE KINASE SUBFAMILY.

-----

THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----

EMBL: U39657; AAC50389.1; -

DR EMBL: U39656; AAC50388.1; -

DR EMBL: U49732; AAB05035.1; -

DR EMBL: U39065; AAB03705.1; -

DR EMBL: U39064; AAB03708.1; -

DR EMBL: D87905; BAA13496.1; -

DR EMBL: X96757; CAA65532.1; -

DR Genew: H96757; MAP2K6.

DR MIM: 601254; -

DR InterPro: IPR000719; Euk\_pkinase.

DR InterPro: IPR002290; Ser\_thr\_pkinase.

DR Pfam: PF000069; pkinase; 1.

DR Prodom: PD000001; Euk\_pkinase; 1.

DR SMART: SM00220; S\_TKc; 1.

DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.

DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.

KW Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;

KW ATP-binding; Phosphorylation; Alternative splicing.

FT DOMAIN 53 314 PROTEIN KINASE.

FT NP\_BIND 59 67 ATP (BY SIMILARITY).

FT BINDING 82 82 ATP (BY SIMILARITY).

FT ACT\_SITE 179 179 BY SIMILARITY.

FT MOD\_RES 207 207 PHOSPHORYLATION (PROBABLE).

FT MOD\_RES 211 211 PHOSPHORYLATION (PROBABLE).

FT SITE 14 15 CLEAVAGE (BY ANTHRAX LETHAL FACTOR).

FT VARSLIC 1 56 MISSING (IN ISOFORM MKK6).

FT MUTAGEN 207 207 S->E: CONSTITUTIVE ACTIVATION ACCORDING

FT MUTAGEN 207 207 TO REF. 1 BUT NOT TO REF. 3.

FT MUTAGEN 211 211 S->A: INACTIVATION.

FT MUTAGEN 211 211 T->E: CONSTITUTIVE ACTIVATION ACCORDING

FT MUTAGEN 211 211 T->E: 1 BUT NOT TO REF. 3.

FT MUTAGEN 211 211 T->A: INACTIVATION.

FT CONFLICT 125 125 V -> M (IN REF. 3).

FT SEQUENCE 334 AA; 37492 MW; 4ECA801522216AF CMC64;

Query Match 100.0%; Score 1731; DB 1; Length 334;

Best Local Similarity 100.0%; Pseud. No. 2.2e-117;

Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SOSGKKRNPGLKIPKAEFEQPTSTPPRLDLSKACISIGNONFEVKADLEPIMLGR 60

|||||

Db 2 SOSGKKRNPGLKIPKAEFEQPTSTPPRLDLSKACISIGNONFEVKADLEPIMLGR 61

QY 61 GAYGVYKKRHVPSGQIMAVKRIATVNSQOKRLMLDLDISMTVDCPFTVYGFALFR 120

Db 62 GAYGVYKKRHVPSGQIMAVKRIATVNSQOKRLMLDLDISMTVDCPFTVYGFALFR 121

QY 121 EGDVWICMELMDTSLDKFYQVYDKQOTIREDILGKIAVSVKALHLSKLSVYHSDVK 180

Db 122 EGDVWICMELMDTSLDKFYQVYDKQOTIREDILGKIAVSVKALHLSKLSVYHSDVK 181

QY 181 PSVVLNAGGVKMCDFGIGYLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIW 240

Db 182 PSVVLNAGGVKMCDFGIGYLVDSVAKTIDAGCKPYMAPERINPELNQKGYSVKSDIW 241

QY 241 SLGITMELALILFPYDSWGTPEQOLKQVVEEPPOLPADKFSAEFVDTSQCLKNKSE 300

Db 242 SLGITMELALILFPYDSWGTPEQOLKQVVEEPPOLPADKFSAEFVDTSQCLKNKSE 301

QY 301 RPTYPELMQHPFTLHESKGTVDVAFVLLIGD 333

Db 302 RPTYPELMQHPFTLHESKGTVDVAFVLLIGD 334

RESULT 2

MPK6\_MOUSE STANDARD; PRT; 334 AA.

ID MPK6\_MOUSE

AC P70236;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Dual specificity mitogen-activated protein kinase kinase 6

DE (EC 2.7.1.1.) (MAP kinase kinase 6) (MAPK 6) (MAPK/ERK kinase 6)

DE (SAPKK3).

GN MAP2K6 OR PRPK6 OR SAPK3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE-97015116; PubMed-8861944;

RA Cuenda A., Alonso G., Morrice N., Jones M., Meler R., Cohen P.,

RA Nebreda A.R.;

RT "Purification and cDNA cloning of SAPK3, the major activator of

RT RK/P38 in stress- and cytokine-stimulated monocytes and epithelial

RT cells."

RL EMBO J. 15:4156-4164(1996).

CC -1- FUNCTION: CATALYZES THE CONCOMITANT PHOSPHORYLATION OF A THREONINE

CC AND A TYROSINE RESIDUE IN MAP KINASE P38 EXCLUSIVELY.

CC -1- ENZYME REGULATION: PROBABLY ACTIVATED BY DUAL PHOSPHORYLATION ON

CC SER-207 AND THR-211 (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC MAP KINASE KINASE SUBFAMILY.

-----

THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

-----

EMBL: X97052; CAA65764.1; -

DR MGD: MGI:1346870; Map2K6.

DR InterPro: IPR000719; Euk\_pkinase.

DR InterPro: IPR002290; Ser\_thr\_pkinase.

DR Pfam: PF000069; pkinase; 1.

DR Prodom: PD000001; Euk\_pkinase; 1.

DR SMART: SM00220; S\_TKc; 1.

DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.

DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.

KW Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;

KW ATP-binding; Phosphorylation. PROTEIN KINASE.  
 FT DOMAIN 53 314  
 FT NP\_BIND 59 67  
 FT BINDING 82 82  
 FT ACT\_SITE 179 179  
 FT MOD\_RES 207 207  
 FT MOD\_RES 211 211  
 SO SEQUENCE 334 AA: 37432 MW: 62CEFC28AF50BAC CRC64;

Query Match 98.5%; Score 1705; DB 1; Length 334;  
 Best Local Similarity 97.9%; Pred. No. 1,6e-115;  
 Matches 326; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 SOSGKKRNPGLIKREAFEPQSTPRDDSKACISIGNONFEVKADDEPIVELGR 60  
 DB 2 SOSGKKRNPGLIKREAFEPQSTPRDDSKACISIGNONFEVKADDEPIVELGR 61  
 QY 61 GAYGVKRRHVPSCQIMAVKRIRATVNSQEQRLMDLDSMRVDCFTVYFALFR 120  
 DB 62 GAYGVKRRHVPSCQIMAVKRIRATVNSQEQRLMDLDSMRVDCFTVYFALFR 121  
 QY 121 EGDVWICMELMDTSLDKFFKQVYDGGOTPEIDILKINATYKALEHLSKLSVHRDYK 180  
 DB 122 EGDVWICMELMDTSLDKFFKQVYDGGOTPEIDILKINATYKALEHLSKLSVHRDYK 181  
 QY 181 PSNVLLNALGOVKMCDGFSIGYLVDSVAKTIDAGCKPYAPRINPELNOKGYSKSDIM 240  
 DB 182 PSNVLLNALGOVKMCDGFSIGYLVDSVAKTIDAGCKPYAPRINPELNOKGYSKSDIM 241  
 QY 241 SLGITMIELATLRPPYDSWGTFFQOLKOVVEPSPQLPADKFSAEFVDTSQCLKNKSE 300  
 DB 242 SLGITMIELATLRPPYDSWGTFFQOLKOVVEPSPQLPADKFSAEFVDTSQCLKNKSE 301  
 QY 301 RPTYPELMOHPEFTVHESKADVASFVKLLIGD 333  
 DB 302 RPTYPELMOHPEFTVHESKADVASFVKLLIGD 334

RESULT 3  
 ID MPK3\_HUMAN STANDARD; PRT; 318 AA.  
 AC P46734;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Dual specificity mitogen-activated protein kinase kinase 3  
 DE (EC 2.7.1.1) (MAP kinase kinase 3) (MAPKK 3) (MAPK/ERR kinase 3).  
 GN MAP2K3 OR PRKMK3 OR MEK3 OR MEK3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA MEDLINE=95141073; Pubmed=7839144;  
 RA Derjard B., Raligeaud J., Barrett T., Wu I.-H., Han J.,  
 RA Ulevitch R.J., Davis R.J.;  
 RT "Independent human MAP-kinase signal transduction pathways defined by  
 RT MEK and MKK isoforms.";  
 RL Science 267:682-685(1995).  
 RN [2]  
 RP MUTAGENESIS.  
 RP MEDLINE=96182129; Pubmed=8622669;  
 RA Raligeaud J., Whitmarsh A.J., Barrett T., Derjard B., Davis R.J.;  
 RT "MKK3- and MKK6-regulated gene expression is mediated by the p38  
 RT Mol. Cell. Biol. 16:1247-1255(1996).  
 CC -1- FUNCTION: DUAL SPECIFICITY KINASE. IS ACTIVATED BY CYTOKINES AND  
 CC ENVIRONMENTAL STRESS IN VIVO. CATALYZES THE CONCOMITANT  
 CC PHOSPHORYLATION OF A THREONINE AND A TYROSINE RESIDUE IN THE MAP  
 CC KINASE P38.  
 CC -1- ENZYME REGULATION: ACTIVATED BY DUAL PHOSPHORYLATION ON SER-189

CC AND THR-193.  
 CC -1- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IS SEEN IN THE SKELETAL  
 CC MUSCLE. IT IS ALSO WIDELY EXPRESSED IN OTHER TISSUES.  
 CC -1- PFM: AUTOPHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: L36719; AAC41718.1;  
 CC Genbank: HGNC:6843; MAP2K3.  
 CC MIM: 602315;  
 CC DR InterPro: IPR000719; Euk\_pkinase.  
 CC DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 CC DR Pfam: PF00069; Pkinase; 1.  
 CC DR ProDom: PD000004; Euk\_Pkinase; 1.  
 CC DR SMART: SM00220; S\_TKc; 1.  
 CC DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC KW ATP-binding; Serine/threonine-protein kinase; Tyrosine-protein kinase;  
 CC ATP-binding; Phosphorylation.  
 CC FT DOMAIN 35 296  
 CC FT NP\_BIND 41 49  
 CC FT BINDING 64 64  
 CC FT ACT\_SITE 161 161  
 CC FT MOD\_RES 189 189  
 CC FT MOD\_RES 193 193  
 CC FT MOD\_RES 189 189  
 CC FT MOD\_RES 193 193  
 CC FT MOTAGEN 193 193  
 CC FT MOTAGEN 193 193  
 CC FT MOTAGEN 193 193  
 CC SO SEQUENCE 318 AA: 36172 MW: 966821BE4B76E0DA CRC64;

Query Match 79.0%; Score 1367; DB 1; Length 318;  
 Best Local Similarity 82.7%; Pred. No. 2.8e-91;  
 Matches 258; Conservative 30; Mismatches 24; Indels 0; Gaps 0;

QY 22 POTSSTPRDDSKACISIGNONFEVKADDEPIVELGRGAYGVKRRHVPSCQIMAVK 81  
 DB 5 PAVNPPRRLDSRTFTTIGDRNFEVADDLVTSISLGRGAYGVKRRHVPSCQIMAVK 64  
 QY 82 RIRATVNSQEQRLMDLDSMRVDCFTVYFALFRGQVWICMELMDTSLDKFFRK 141  
 DB 65 RIRATVNSQEQRLMDLDSMRVDCFTVYFALFRGQVWICMELMDTSLDKFFRK 124  
 QY 142 VIDKGTPEIDILKINATYKALEHLSKLSVHRDYKPSNVLLNALGOVKMCDGFSIG 201  
 DB 125 VIDKMTPEIDILKINATYKALEHLSKLSVHRDYKPSNVLLNALGOVKMCDGFSIG 184  
 QY 202 YLVDSVAKTIDAGCKPYAPRINPELNOKGYSKSDIMSLGITMIELATLRPPYDSWGT 261  
 DB 165 YLVDSVAKTIDAGCKPYAPRINPELNOKGYSKSDIMSLGITMIELATLRPPYDSWGT 244  
 QY 262 PEOOLKOVVEPSPQLPADKFSAEFVDTSQCLKNKSEKPTYPELMOHPEFTVHESKGT 321  
 DB 245 PEOOLKOVVEPSPQLPADKFSAEFVDTSQCLKNKSEKPTYPELMOHPEFTVHESKGT 304  
 QY 322 DVASFVKLLIGD 333  
 DB 305 DVASFVKLLIGD 316

RESULT 4  
 ID MPK3\_MOUSE STANDARD; PRT; 314 AA.  
 AC O09110;

DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Dual specificity mitogen-activated protein kinase 3  
 DE (EC 2.7.1.1-) (MAP kinase kinase 3) (MAPKK 3) (MAP/ERK kinase 3).  
 GN MAP2K3 OR PRKMK3 OR MKK3.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Neuhinger A., Gaestel M.;  
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.  
 CC -1 FUNCTION: DUAL SPECIFICITY KINASE. IS ACTIVATED BY CYTOKINES AND  
 CC ENVIRONMENTAL STRESS IN VIVO. CATALYZES THE CONCOMITANT  
 CC PHOSPHORYLATION OF A THREONINE AND A TYROSINE RESIDUE IN THE MAP  
 CC KINASE P38 (BY SIMILARITY).  
 CC -1 ENZYME REGULATION: ACTIVATED BY DUAL PHOSPHORYLATION ON SER-185  
 CC AND THR-189 (BY SIMILARITY).  
 CC -1 PFM: AUTOPHOSPHORYLATED.  
 CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sb.ch](mailto:license@sib-sb.ch)).  
 CC -----  
 CC EMBL: X93150; CAA63649.1; -  
 CC DR MGD; MG1:1346868; Map2k3.  
 CC DR InterPro: IPR000719; Euk\_pkinase.  
 CC DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 CC DR Pfam: PF00069; pkinase; 1.  
 CC DR ProDom: PD000001; Euk\_pkinase; 1.  
 CC DR SMART; SM00220; S\_TKc; 1.  
 CC DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC KW Transferrase; Serine/threonine-protein kinase; Tyrosine-protein kinase;  
 CC ATP-binding; Phosphorylation.  
 CC FT DOMAIN 31 292 PROTEIN KINASE.  
 CC FT NP\_BIND 37 45 ATP (BY SIMILARITY).  
 CC FT BINDING 60 60 ATP (BY SIMILARITY).  
 CC FT ACT\_SITE 157 157 BY SIMILARITY.  
 CC FT MOD\_RES 185 185 PHOSPHORYLATION.  
 CC FT MOD\_RES 189 189 PHOSPHORYLATION.  
 CC FT MOD\_RES 189 189 PHOSPHORYLATION.  
 CC SO SEQUENCE 314 AA; 35883 MW; 9D60CA9180AE7B4A CRC64;  
 Query Match 77.1%; Score 1334; DB 1; Length 314;  
 Best Local Similarity 82.7%; Pred. No. 6.4e-89;  
 Matches 253; Conservative 29; Mismatches 24; Indels 0; Gaps 0;  
 OY 28 PPRLDLSKACISIGNQNEFYKADLEPIMELRGAGYVEKRRHVPSCQIMAVKRIRATV 87  
 DB 7 PPNLIDSRITITIGDRNFEVKADLVITISELRCAGYVEKRRHVPSCQIMAVKRIRATV 66  
 OY 88 NSQDQKRLMDLISMTVDCPTVTYFGALFRGSDWICMLMDTSLDKFYKQYIDVSGQ 147  
 DB 67 NFOEQKRLMDLIDMTVDCPTVTYFGALFRGSDWICMLMDTSLDKFYKQYIDVSGQ 126  
 OY 148 TTPEDILGKIAVSIVKALEHLSKLSVLRDVKPSNVLLNALGVKMCDFGISGLYVDSV 207  
 DB 127 KIPEDILGKIAVSIVKALEHLSKLSVLRDVKPSNVLLINRGHKKMCDGFGISGLYVDSV 186  
 OY 208 AKTIDACKPYMAERINPELNOKGYSVKSDIWSLGTIMELAILRFYDMSGTFPQDLK 267  
 DB 187 AKTMDACKPYMAERINPELNOKGYSVKSDIWSLGTIMELAILRFYDMSGTFPQDLK 246  
 OY 268 QVEEPPSQLPADKFAEFVFTSGCLKKSKERERTYELMQHPFTLHESGTDVASFV 327

DB 247 QVEEPPSQLPADKFAEFVFTSGCLKKSKERERTYELMQHPFTLHESGTDVASFV 306  
 OY 328 KLILCD 333  
 DB 307 KETLGE 312  
 RESULT 5  
 MPK2\_XENLA STANDARD; PRT; 446 AA.  
 ID MPK2\_XENLA  
 AC 007192;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Dual specificity mitogen-activated protein kinase 2  
 DE (EC 2.7.1.1-) (MAP kinase kinase 2) (MAPKK 2) (MAP/ERK kinase 2)  
 DE (fragment).  
 GN MEK2.  
 OS Xenopus laevis (African clawed frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 CC Xenopodinae; Xenopus.  
 CC NCBI\_TaxID=8353;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE-Embryo;  
 RL MEDLINE-93361007; Pubmed-8395011;  
 RA Yashar B.M., Kelley C., Yee K., Errede B., Zon L.I.;  
 RT "Novel members of the mitogen-activated protein kinase activator  
 RT family in Xenopus laevis".  
 RT Mol. Cell. Biol. 13:5738-5748(1993).  
 CC -1 FUNCTION: CATALYZES THE CONCOMITANT PHOSPHORYLATION OF A THREONINE  
 CC AND A TYROSINE RESIDUE IN A THR-GLU-TYR SEQUENCE LOCATED IN MAP  
 CC KINASES.  
 CC -1 ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be  
 CC produced by alternative splicing.  
 CC -1 TISSUE SPECIFICITY: IS EXPRESSED ABUNDANTLY IN THE ADULT  
 CC BRAIN AND MUSCLE.  
 CC -1 DEVELOPMENTAL STAGE: IT IS INITIALLY EXPRESSED IN THE DORSAL  
 CC REGION OF THE EMBRYO IN A DIFFUSE PATTERN AT STAGE 17.  
 CC SUBSEQUENTLY EXPRESSION OCCURS IN THE EARLY STAGES OF DEVELOPMENT  
 CC OF THE CENTRAL NERVOUS SYSTEM, INCLUDING THE BRAIN, SPINAL CORD  
 CC AND EYE. LATER (STAGE 24) EXPRESSION IS FOUND IN THE HINDBRAIN,  
 CC MIDBRAIN AND FOREBRAIN AND THE SOMITES. BY STAGE 32, THE  
 CC EXPRESSION IS DETECTED IN THE CRANIAL NERVOUS. EXPRESSION IN THE  
 CC BRAIN IS INCREASED, WHILE EXPRESSION IN THE SPINAL CORD HAS  
 CC DECREASED BY STAGE 37.  
 CC -1 PFM: MAPK IS ITSELF DEPENDENT ON SER/THR PHOSPHORYLATION FOR  
 CC ACTIVITY CATALYZED BY MAP KINASE KINASES (RAV).  
 CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sb.ch)).  
 CC -----  
 CC EMBL: Z22736; CAA80430.1; -  
 CC DR InterPro: IPR000719; Euk\_pkinase.  
 CC DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 CC DR Pfam: PF00069; pkinase; 1.  
 CC DR ProDom: PD000001; Euk\_pkinase; 1.  
 CC DR SMART; SM00220; S\_TKc; 1.  
 CC DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC KW Transferrase; Serine/threonine-protein kinase; Tyrosine-protein kinase;  
 CC ATP-binding; Phosphorylation; Alternative splicing.  
 CC FT NON\_TER 1 1



FT DOMAIN 22 40 SER-RICH.  
 FT DOMAIN 149 414 PROTEIN KINASE.  
 FT NP\_BIND 155 163 ATP (BY SIMILARITY).  
 FT BINDING 178 178 ATP (BY SIMILARITY).  
 FT ACT\_SITE 276 276 BY SIMILARITY.  
 FT MOD\_RES 304 304 PHOSPHORYLATION (BY RAF) (BY SIMILARITY).  
 FT MOD\_RES 308 308 PHOSPHORYLATION (BY RAF) (BY SIMILARITY).  
 FT VARSPLIC 51 51 G->GLIINCDNMQS (IN ISOFORM 2).  
 FT MUTAGEN 178 178 K->R: LOSS OF ACTIVITY.  
 SQ SEQUENCE 446 AA; 50100 MW; 9E6B5DCAD0695662 CRC64.

Query Match 53.4%; Score 924.5; DB 1; Length 446;  
 Best Local Similarity 53.4%; Pred. No. 2.4e-59;  
 Matches 183; Conservative 51; Mismatches 92; Indels 17; Gaps 5;

QY 1 SOSKGRKRPGLK-----IPKFAFOPPSPPRDLDSKACISIG-NQNEFKADL 52  
 DB 95 SYGKODLRITGCAALSTNEQATNRLERLTHS-----IESGKLUKISPEQHWDTADL 149  
 QY 53 EPIMEIGRGAYGVYKMRHVPSSQIMAVKRIRATVNSOEOKRLMDIDISMRVDCPPTV 112  
 DB 150 KDLGEIRGAYGVYKMRHVPSSQIMAVKRIRATVNSOEOKRLMDIDLVVRRSDCPYIV 209  
 QY 113 TFGALFREDGVCICMELMDTSIDKFKYKVID-KGOTIPEDILKIAVSIKALEHHSK 171  
 DB 210 QFTGALFREDGVCICMELMDTSIDKFKYKVID-KGOTIPEDILKIAVSIKALEHHSK 269  
 QY 172 LSVIHRDVPKPSNVLYNALGVKMDGFGISGYLVDSVAKTIDAGCKPYMAPERINDELNOK 231  
 DB 270 LKTIHRDIPKPSNVLYNALGVKMDGFGISGYLVDSVAKTIDAGCKPYMAPERINDELNOK 329  
 QY 232 GYSVSDISLGTITMELALIRPPYDSWGPFOQLKOVVEEPSPOLPAD--KFSAEFVD 288  
 DB 330 GYDVRSDVSLGTITMELALIRPPYDSWGPFOQLKOVVEEPSPOLPAD--KFSAEFVD 389  
 QY 289 FTSOCLKNSKERPTYPELMOPHFTLHESKGTDVASFVKLL 331  
 DB 390 FYNQCLTKDESKRPKYLKHPFLIMTEERTVDVAGYVKIL 432

RESULT 6  
 MPK4\_MOUSE STANDARD; PRT; 397 AA.

AC P47809;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Dual specificity mitogen-activated protein kinase kinase 4  
 DE (EC 2.7.1.-) (MAP kinase kinase 4) (MAPK 4) (MAPK/ERK kinase 4) (JNK activating kinase 1) (C-JUN N-terminal kinase kinase 1) (JNK kinase 1)  
 DE (JUNK 1) (SAPK/ERK kinase 1) (SEK1)  
 GN MAP2K4 OR PRKMK4 OR JUNK1 OR SEK1 OR SEK1.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=95089821, PubMed=7997269;  
 RA Sanchez I., Hughes R.T., Mayer B.J., Yee K., Woodgett J.R., Avruch J., Kyriakis J.M., Zon L.I.;  
 RT "Role of SAPK/ERK kinase-1 in the stress-activated pathway regulating transcription factor c-Jun.";  
 RT Nature 372:794-798(1994).  
 RL [2]  
 RP REVISIONS.  
 RA Zon L.I.;  
 RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: DUAL SPECIFICITY KINASE THAT ACTIVATES THE JUN KINASES MAPK8 (JNK1) AND MAPK9 (JNK2) AS WELL AS MAPK14 (P38) BUT NOT MAPK1 (ERK2) OR MAPK3 (ERK1).  
 CC -1- TISSUE SPECIFICITY: IS EXPRESSED ABUNDANTLY IN THE ADULT

CC BRAIN AND MUSCLE.  
 CC -1- P-TM: ACTIVATED BY PHOSPHORYLATION ON SER/THR BY MAP KINASE KINASE KINASES (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: U18310; AAB1554.1; -  
 DR MGI: MGI:1346869; Map2k4.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase.1.  
 DR ProDom: PD000001; Euk\_pkinase.1.  
 DR SMART: SM00220; S\_TKc.1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_AAP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transferase: Serine/threonine-protein kinase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.  
 KW DOMAIN 5  
 KW NP\_BIND 100  
 KW BINDING 103  
 KW ACT\_SITE 129  
 KW MUTAGEN 129  
 KW SEQUENCE 397 AA; 44113 MW; B9C6688184E53D CRC64;

Query Match 53.1%; Score 920; DB 1; Length 397;  
 Best Local Similarity 51.6%; Pred. No. 4.4e-59;  
 Matches 182; Conservative 57; Mismatches 90; Indels 24; Gaps 6;

QY 1 SOSKGRKRPGLK-----NPKGIRKPEAQEQTSSTP-----PRDLDSKACISIG-NQNEFKADL 44  
 DB 33 SMOGRKRLKLNFPANPPKYSTARFTLNTNTGVONPHIERLTHSIESGKLUKISPEQH 92  
 QY 45 FEVKADDELEPIMELRGAYGVYKMRHVPSSQIMAVKRIRATVNSOEOKRLMDIDISMR 104  
 DB 93 WDFTEDELKDLGEIRGAYGVYKMRHVPSSQIMAVKRIRATVNSOEOKRLMDIDLVVRR 152  
 QY 105 TVDCEFTYTFGALFREDGVCICMELMDTSIDKFKYKVID-KGOTIPEDILKIAVSI 161  
 DB 153 SSDDPYIVQFYGALFREDGVCICMELMDTSIDKFKYKVID-KGOTIPEDILKIAVSI 210  
 QY 162 VKALEHLHSKLSVHRDVPKPSNVLYNALGVKMDGFGISGYLVDSVAKTIDAGCKRYMAP 221  
 DB 211 VKALNHLKENLKIHRDIPKPSNVLYNALGVKMDGFGISGYLVDSVAKTIDAGCKRYMAP 270  
 QY 222 ERINDELNOQGYSVKSDISLGTITMELALIRPPYDSWGPFOQLKOVVEEPSPOLPAD- 280  
 DB 271 ERIDPSASRGQYDVRSDVSLGTITMELALIRPPYDSWGPFOQLKOVVEEPSPOLPAD- 330  
 QY 281 --KFSAEFVDTSOCLKNSKERPTYPELMOPHFTLHESKGTDVASFVKLL 331  
 DB 331 ERFSPSPFINVNLCTLTKDESKRPKYLKHPFLIMTEERTVDVAGYVKIL 383

RESULT 7  
 MPK4\_HUMAN STANDARD; PRT; 399 AA.

AC P45985;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Dual specificity mitogen-activated protein kinase kinase 4  
 DE (EC 2.7.1.-) (MAP kinase kinase 4) (JNK activating kinase 1) (C-JUN N-terminal kinase kinase 1) (JUNK) (SAPK/ERK kinase 1) (SEK1).

GN MAP2K4 OR PRKMK4 OR JNK1 OR MKK4 OR SEKK1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9523504; PubMed=7716521;  
 RA Lin A., Minden A., Martinetto H., Claret F.-X., Lange-Carter C.,  
 Mercurio F., Johnson G.L., Karin M.,  
 RT "Identification of a dual specificity kinase that activates the Jun  
 RT kinases and p38-Mpk2."  
 RL Science 268:286-290(1995).  
 RN  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=95141073; PubMed=7839144;  
 RA Derjard B., Ransgaard J., Barrett T., Wu I.-H., Han J.,  
 RT Ulevitch R.J., Davis R.J.;  
 RT "Independent human MAP-kinase signal transduction pathways defined by  
 RT MEK and MKK isoforms."  
 RL Science 267:682-685(1995).  
 RN  
 [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98283589; PubMed=9622070;  
 RA Su G.H., Hlgers W., Shekher M.C., Tang D.J., Yeo C.J., Hruban R.H.,  
 RT Kern S.E.;  
 RT "Alterations in pancreatic, biliary, and breast carcinomas support  
 RT MKK4 as a genetically targeted tumor suppressor gene."  
 RL Cancer Res. 58:2339-2342(1998).  
 RN  
 [4]  
 RP CLEAVAGE BY ANTHRAX LETHAL FACTOR.  
 RX MEDLINE=20558083; PubMed=11104681;  
 RA Vitale G., Bernadil L., Napolitano G., Mock M., Montecucco C.;  
 RT "Susceptibility of mitogen-activated protein kinase family  
 RT members to proteolysis by anthrax lethal factor."  
 RL Biochem. J. 382:739-745(2000).  
 CC  
 -1- FUNCTION: DUAL SPECIFICITY KINASE THAT ACTIVATES THE JUN KINASES  
 CC MARK8 (JNK1) AND MARK9 (JNK2) AS WELL AS MARK14 (P38) BUT NOT  
 CC MARK1 (ERK2) OR MARK3 (ERK1).  
 CC -1- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IS SEEN IN THE SKELETAL  
 CC MUSCLE. IT IS ALSO WIDELY EXPRESSED IN OTHER TISSUES.  
 CC -1- PTM: ACTIVATED BY PHOSPHORYLATION ON SER/THR BY MAP KINASE KINASE  
 CC KINASES (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -1- MAP KINASE KINASE SUBFAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: U17743; AAC50127.1; -  
 DR EMBL: L36870; AAC41719.1; -  
 DR EMBL: AF070090; AAC24130.1; -  
 DR EMBL: AF070080; AAC24130.1; JOINED.  
 DR EMBL: AF070081; AAC24130.1; JOINED.  
 DR EMBL: AF070082; AAC24130.1; JOINED.  
 DR EMBL: AF070083; AAC24130.1; JOINED.  
 DR EMBL: AF070084; AAC24130.1; JOINED.  
 DR EMBL: AF070085; AAC24130.1; JOINED.  
 DR EMBL: AF070086; AAC24130.1; JOINED.  
 DR EMBL: AF070087; AAC24130.1; JOINED.  
 DR EMBL: AF070088; AAC24130.1; JOINED.  
 DR EMBL: AF070089; AAC24130.1; JOINED.  
 DR GeneW: HGNC:6844; MAP2K4.  
 DR MIM: 601335; -  
 DR InterPro: IPR000719; Euk\_kinase.  
 DR InterPro: IPR002290; Ser\_thr\_kinase.  
 DR Pfam: pf00069; kinase; 1.

DR ProDom: PD0000001; Euk\_kinase; 1.  
 DR SMART: SM00220; S\_TKc.1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;  
 KW ATP-binding; Phosphorylation.  
 FT DOMAIN 5 19 GLY/SER-RICH.  
 FT DOMAIN 102 367 PROTEIN KINASE.  
 FT NP\_BIND 105 113 ATP (BY SIMILARITY).  
 FT BINDING 131 131 ATP (BY SIMILARITY).  
 FT ACT\_SITE 229 229 BY SIMILARITY.  
 FT SITE 45 46 CLEAVAGE (BY ANTHRAX LETHAL FACTOR).  
 FT SITE 58 59 CLEAVAGE (BY ANTHRAX LETHAL FACTOR).  
 FT SITE 59 59  
 SQ SEQUENCE 399 AA; 44287 MW; A472537EF26770B CRC64;  
 Query Match 53.18; Score 919; DB 1; Length 399;  
 Best Local Similarity 51.38; Pred. No. 5.3e-59;  
 Matches 181; Conservative 56; Mismatches 92; Indels 24; Gaps 6;  
 OY 1 SQSGKKR-----NFKLTKPK-----AFEPQTSSTPPRDIDSKACISIG-NQN 44  
 DB 35 SSMQGRKALKLNFPANPFKSTARFLNPNPTGVQNPRIERLRTHSIESGKLKISPEQH 94  
 OY 45 FEVKADDEPIMELGRCAYGVVEKMRHVPSCQIMAVKRIATVNSQEQRLMDIDSMR 104  
 DB 95 WDFLAEDLKDGLGEIGRCAYGVVNMKHPSCQIMAVKRIATVDEKEQKQLMDIDVVR 154  
 OY 105 TVDCPFVTVYTGALFRGSDWICMEIMDTSIDKRYK--QYIDKQGITPEDILKIAVSI 161  
 DB 155 SSDCPYVQFYGALFRGSDWICMEIMDTSIDKRYKYVSLD--DYIPEILGKITLTAT 212  
 OY 162 VKALEHLSKLSVYHRDVPKPSNVLMALGVKMGDFGISGLVDSVAKTIDAGCKPYAP 221  
 DB 213 VKALNHLEKMKIITHROIKPNSILLDRSGNIKLCDFGISGLVDSIAKTRAGCRRYAP 272  
 OY 222 ERINPELNQKSYKSDWSIGIMIELAIRFPVDSMGTPPOOLKOVVEEPPSLPAD- 280  
 DB 273 ERIDPSASRQGYDVRSDWSIGITLYELAEFRFPKPNKNSVPDQLQYVKGQPPDLSNE 332  
 OY 281 --KFSAEVDFTSOCLKKNKSRPTYPPELMQHPFTLESKTDVAASFVKIL 331  
 DB 333 ERESPTINVINCLTDESKRPYKELKNPFLIMEERAVEACVCKIL 385  
 RESULT 8  
 ID MPK7\_HUMAN STANDARD; PRT; 419 AA.  
 AC Q14733; Q14648; O60452; O60453; Q14816;  
 DT 30-MAY-2000 (Rel. 39; Created)  
 DT 30-MAY-2000 (Rel. 39; Last sequence update)  
 DT 15-JUN-2002 (Rel. 41; Last annotation update)  
 DE Dual specificity mitogen-activated protein kinase kinase 7  
 DE (EC 2.7.1.-) (MAP kinase kinase 7) (MAPKK 7) (MAPK/ERK kinase 7) (JNK  
 DE activating kinase 2) (C-Jun N-terminal kinase kinase 2) (JNK kinase 2)  
 DE (JUNK 2).  
 GN MAP2K7 OR PRKMK7 OR JNK2 OR MKK7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle, and Heart;  
 RX MEDLINE=98038808; PubMed=9372971;  
 RA Wu Z., Wu J., Jacinto E., Karin M.;  
 RT "Molecular cloning and characterization of human JNK2, a novel Jun  
 RT NH2-terminal kinase-specific kinase."  
 RL Mol. Cell. Biol. 17:7407-7416(1997).  
 RN  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97460048; PubMed=9312068;  
 RA Lu X., Nemoto S., Lin A.;

RT "Identification of c-Jun NH2-terminal protein kinase (JNK)-activating  
 RT kinase 2 as an activator of JNK but not p38.";  
 RL J. Biol. Chem. 272:24751-24754(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=98204938; PubMed=9535930;  
 RA Foltz I.N., Gerl R.E., Wietler J.S., Luckach M., Salmon R.A.,  
 RA Schrader J.W.;  
 RT "Human mitogen-activated protein kinase 7 (MK7) is a highly  
 RT conserved c-Jun N-terminal kinase/stress-activated protein kinase  
 RT (JNK/SAPK) activated by environmental stresses and physiological  
 RT stimuli.";  
 RL J. Biol. Chem. 273:9344-9351(1998).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Yang J., New L., Yong J., Han J., Su B.;  
 RT "Molecular cloning of human JNK2 reveals a novel kinase module for  
 RT c-Jun N-terminal kinase activation";  
 RL Submitted (Sep-1997) to the EMBL/Genbank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 1-260 FROM N.A.  
 RX MEDLINE=97352799; PubMed=9207092;  
 RA Tourlier C., Whitmarsh A.J., Cavanagh J., Barrett T., Davis R.J.;  
 RT "Mitogen-activated protein kinase 7 is an activator of the c-  
 RT Jun NH2-terminal kinase.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:7337-7342(1997).  
 RN [6]  
 RP CLEAVAGE BY ANTHRAX LETHAL FACTOR.  
 RX MEDLINE=20558083; PubMed=11104681;  
 RA Vitale G., Bernardi L., Napolitani G., Mock M., Montecucco C.;  
 RT "Susceptibility of mitogen-activated protein kinase kinase family  
 RT members to proteolysis by anthrax lethal factor.";  
 RL Biochem. J. 352:739-745(2000).  
 CC -1- FUNCTION: DUAL SPECIFICITY KINASE THAT ACTIVATES THE JUN KINASES  
 CC MAPK8 (JNK1) AND MAPK9 (JNK2).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A (SHOWN HERE) AND B; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: UBQUITOUS; WITH HIGHEST LEVEL OF EXPRESSION  
 CC IN SKELETAL MUSCLE.  
 CC -1- PTM: ACTIVATED BY PHOSPHORYLATION ON SER/THR BY MAP KINASE KINASE  
 CC KINASES (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: AF014401; AAB88048.1; -;  
 DR EMBL: AF006689; AAB97813.1; ALT\_TERM.  
 DR EMBL: AF013588; AAC16272.1; -;  
 DR EMBL: AF013589; AAC16273.1; -;  
 DR EMBL: AF022805; AAC26142.1; -;  
 DR EMBL: AF003199; AAB63374.1; -;  
 DR Genew: HGNC:6847; MAP2K7.  
 DR MIM: 603014; -;  
 DR InterPro: IPR000719; Euk\_kinase.  
 DR InterPro: IPR002290; Ser\_thr\_kinase.  
 DR Pfam: PF00069; kinase; 1.  
 DR PiroDom: PD000001; Euk\_kinase; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; FALSE\_NEG.  
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.  
 DR PROSITE: PS0011; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;  
 KW ATP-binding; Phosphorylation; Alternative splicing.  
 FT DOMAIN 120 380  
 FT NP\_BIND 126 134  
 FT ATP (BY SIMILARITY).  
 FT BINDING 149 149  
 FT ATP (BY SIMILARITY).

FT ACT\_SITE 243 243 BY SIMILARITY.  
 FT SITE 44 45 CLEAVAGE (BY ANTHRAX LETHAL FACTOR).  
 FT SITE 76 77 CLEAVAGE (BY ANTHRAX LETHAL FACTOR).  
 FT VARSPIC 111 111  
 FT CONFLICT 94 94  
 FT CONFLICT 133 133  
 FT CONFLICT 142 142  
 FT CONFLICT 259 259  
 SQ SEQUENCE 419 AA; 47485 MW; F1B22E05F54299A CMC64;  
 Query Match 40.38; Score 697; DB 1; Length 419;  
 Best Local Similarity 42.98; Pred. No. 48e-43;  
 Matches 148; Conservative 69; Mismatches 110; Indels 18; Gaps 7;  
 QY 1 SOSGKRRNPGLIKPEAFPOPTSPPR---DLQSK-----ACISIGNNEVVK 48  
 Db 58 SESSPQHPPPAR-PRMGLPLSTLPPRSMESIEIDKLOEIMKQGYLTIGQRYOAE 116  
 QY 49 ADLEPIMELGRAGYVERKRRHPVSGQIMAVKRIRATVNSQEQRLIMDDISMRVDC 108  
 Db 117 INLEMLGEMSGTCGQVMMKRRKTHVIAVKQRRSGKNEKKRILMDLVYKSHDC 176  
 QY 109 PFTVTFYCALFRGSDWICHELMDISDKRYKQYIDKQGTIPEDILGKIAVSYKALEHL 168  
 Db 177 PIVQCFGFTITWDFIAELMGTCAEKLKKRM--OG-DIPERILKMTVAIVKALYYL 233  
 QY 169 HSKLSYIHRDVKPSNVLINALGVKMDGFSIGLVDSVAKTIDAGCKPWPAPRRIN-PE 227  
 Db 234 KEHGVIHHDVKNRNSLIDBERGQIKLCDFEISGRIDSKAKTSAGCAATAPRIDPDP 293  
 QY 228 LMKGYSVSDWSLITMIEIALILRPYDSWGTPEQOLKQVVEPSPOLPADK-FAEAF 286  
 Db 294 PTKPDIDRADVWSLISIVELATGQFPYKNCXTDFELTKVLOEPPPLLPJGHMGFGDF 353  
 QY 287 VQFTSQCLKNKSEKRPTEYELMHPFTLHESGTVASVXKL 331  
 Db 354 QSFVADCLTKDKRRKRRKIKLHSHFKRYETLEVDAVSWFKDVM 398  
 RESULT 9  
 HEP\_DROME  
 ID HEP\_DROME STANDARD; PRT; 487 AA.  
 AC 023977;  
 DT 01-NOV-1997 (rel. 35, Created)  
 DT 01-NOV-1997 (rel. 35, Last sequence update)  
 DT 30-MAY-2000 (rel. 39, Last annotation update)  
 DE Dual specificity mitogen-activated protein kinase kinase hemipterous  
 DE (EC 2.7.1.-) (MAPKK).  
 OS HEP OR HEM.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Braachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Oregon-R;  
 RX MEDLINE=96067643; PubMed=8521475;  
 RA Glise B., Bourbon H., Noselli S.;  
 RT "Hemipterous encodes a novel Drosophila MAP kinase kinase, required  
 RT for epithelial cell sheet movement.";  
 RL Cell 83:451-461(1995).  
 CC -1- FUNCTION: REQUIRED FOR THE EPITHELIAL CELL SHEET MOVEMENT CALLED  
 CC DORSAL CLOSURE (DC), WHICH ALLOWS ESTABLISHMENT OF THE DORSAL  
 CC EPIDERMIS. CONTROLS THE EXPRESSION IN THE DORSAL EPITHELIUM EDGES  
 CC OF ANOTHER DORSAL CLOSURE GENE, PUCKERED (PUC).  
 CC -1- PTM: MAPK IS ITSELF DEPENDENT ON SER/THR PHOSPHORYLATION FOR  
 CC ACTIVITY CATALYZED BY MAP KINASE KINASE KINASES (BY SIMILARITY).  
 CC -1- PTM: WEAKLY AUTOPHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

DR EMBL: U05240; AAC46944.1; .  
 DR ProBase: FB90010303; hep.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transferase: Serine/threonine-protein kinase; Tyrosine-protein kinase;  
 KW ATP-binding; phosphorylation; Developmental protein.  
 FT DOMAIN 95 106  
 FT NP\_BIND 201 209 ATP (BY SIMILARITY).  
 FT BINDING 224 224 ATP (BY SIMILARITY).  
 FT ACT\_SITE 318 318 BY SIMILARITY.  
 FT MOD\_RES 346 346 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 350 350 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 487 AA; 53079 MW; 09E248DBD14A1E45 CRC64;

Query Match 40.2%; Score 696; DB 1; Length 487;  
 Best Local Similarity 44.2%; Pred. No. 6.8e-43;  
 Matches 141; Conservative 58; Mismatches 100; Indels 20; Gaps 5;

27 TPRPD-----LDKACISIGNQNEFKADLEPIMLGAGVGMKRVPS 74  
 158 TPHPVSEFTMKKLTIMQGTGLNKGQIPYDINDLKLGLGKTSNVYKMHLS 217  
 75 GOIMAVKIRATVNSOEKRLMDLDSMTVDCPTVTFYGLAFREGDVWICMELMDS 134  
 218 NTIIVKQMRKTGMAENKRLMDLVVLKSHDCKIVKCLGCFVRDPDVWICMELMSMC 277  
 135 LDKFKQVINDKQGTIPEDILKAVSIVKALEHLSKLSYIHRDVPSNVLINAGVYM 194  
 278 FPKLKL--LSK--KPVPEQILGKVTAVNALSTLKKGHGIHRDVKSNLLIDRGNIKL 334  
 195 CGEFTSGVLYDSVAKTIDAGCKRYMAPERINPELNOGYSVKSIDMSLITMELALRF 254  
 335 CGFTISGRLYDSKANTRSAGCAAYMAPERIDPK--KPKYDIDVWMLGITIVELATARS 392  
 255 PYDSWGTTPQOLKQVVEEPPQLPADK---FSAEYVDFTSQCLKSKSKERTYBELMQHP 311  
 393 PREGCWTDFEVLTKVLDSEPPCLPYGEGYMFSDQFDFVAKILTKNHQDRKYPBELLAP 452  
 312 FTFLHESKGDVASFVKLI 330  
 453 FRIYESAAYVPMWFOSTI 471

RESULT 10  
 YR62\_CAEEL STANDARD; PRT; 363 AA.  
 ID YR62\_CAEEL 020347; 001707;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE putative serine/threonine-protein kinase F42G10.2 in chromosome II  
 DE (EC 2.7.1.1).  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peleodermidae; Caenorhabditis.  
 OC NCBI\_TaxID-6239;  
 RX [1]  
 RN SEQUENCE FROM N.A.

RC STRAIN-Bristol N2;  
 RA Harris B., Lennard N.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE SUBFAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

DR EMBL: Z95122; CAB08355.1; .  
 DR EMBL: Z48230; CAB08355.1; JOINED.  
 DR EMBL: Z48230; CAB08264.1; .  
 DR EMBL: Z95122; CAB08264.1; JOINED.  
 DR WormPep: F42G10.2; CE10328.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;  
 KW ATP-binding.  
 FT DOMAIN 66 330  
 FT NP\_BIND 72 80 ATP (BY SIMILARITY).  
 FT BINDING 95 95 ATP (BY SIMILARITY).  
 FT ACT\_SITE 194 194 BY SIMILARITY.  
 SQ SEQUENCE 363 AA; 41197 MW; 643A26A23329759A CRC64;

Query Match 36.3%; Score 628.5; DB 1; Length 363;  
 Best Local Similarity 39.8%; Pred. No. 3.4e-38;  
 Matches 136; Conservative 56; Mismatches 111; Indels 39; Gaps 7;

21 QPQTSSTPPRLDLSKACISIGNQ-----FEVADLEPI 56  
 16 RPTSLSTRPTSLSVN-----GNEKTLPEESVLRSLSTGLKPPDEHLYTSSANLQDGL 70  
 57 ELGGVAVGVEMKRVHPGQIMAVKIRATVNSOEKRLMDLDSMTVDCPTVTFY 115  
 71 AIGMGNFTVTKMKRKETGKILAVKRICNNNGHEQRLLEHDPITVSEKGNIVKEY 130  
 116 GAFREGDVWICMELMDSLDEKYQV-IDKQGTIPEDILKAVSIVKALEHLSKLSY 174  
 131 GAFSEGDVWICMELMDSMDLKYRVYVWKNRSLNENYGHITVCTYDALDYLKELKI 190  
 175 IHRDVKPSNVLINAGVYKMCDEFTSGVLYDSVAKTIDAGCKRYMAPERINPELNOGYS 234  
 191 IHRDVKPSNVILVDGVAVALCDFGICGQLEESFAKTHDAGCQPYLAPEKIT---SSDKYD 247  
 235 VKSDIWSLGITMIELALIRFPYDSWGTTPQOLKQVVEEPPQLPADK---FSAEYVDF 290  
 248 VASDVMWSLGITLYELATGKFPYQEWMSLFDQATVAVSGDPIIHPDSDFHYSILPVKEL 307  
 291 SCLKSKSKERTYBELMQHPFTFLHESKGDVASFVKLI 332  
 308 NTLTKRHRHREKPYDLTKSFDYRIYAVAGPEIEE-AKRILG 348

RESULT 11  
 WIS1\_SCHPO STANDARD; PRT; 605 AA.  
 ID WIS1\_SCHPO 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE protein kinase wisi (EC 2.7.1.1) (protein kinase sty2).  
 DE WIS1 OR SPC2 OR STY2 OR SPC409.07C.  
 OS Schizosaccharomyces pombe (fission yeast).



RP SEQUENCE OF 91-101 FROM N.A., AND MUTAGENESIS.  
 RX MEDLINE=95350642; PubMed=7624781;  
 RA Maeda T., Takekawa M., Saito H.;  
 RT "Activation of yeast Pbs2 MAPK by MAPKKs or by binding of an SH3-  
 RL containing osmosensor.";  
 RL Science 269:554-558(1995).  
 RN (5)  
 RP FUNCTION.  
 RX MEDLINE=93206121; PubMed=7681220;  
 RA Brewster J.L., de Valoir T., Dwyer N.D., Winter E., Gustin M.C.;  
 RT "An osmosensing signal transduction pathway in yeast.";  
 RL Science 259:1760-1763(1993).  
 CC -1- FUNCTION: KINASE INVOLVED IN A SIGNAL TRANSDUCTION PATHWAY THAT IS  
 CC ACTIVATED BY CHANGES IN THE OSMOLARITY OF THE EXTRACELLULAR  
 CC ENVIRONMENT. SEEMS TO PHOSPHORYLATE HOG1 ON A TYROSINE RESIDUE.  
 CC -1- DOMAIN: ALTERNATIVE WAY OF ACTIVATION INVOLVES BINDING THE  
 CC PROLINE-RICH MOTIF TO THE SH3 DOMAIN OF SHO1.  
 CC -1- PTM: ACTIVATED BY PHOSPHORYLATION BY SSK2 OR SSK22. SER/THR  
 CC PHOSPHORYLATION IS ALSO NECESSARY FOR SHO1-MEDIATED ACTIVATION.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: J02946; AAA16819.1; -  
 DR EMBL: U12237; AAA20392.1; -  
 DR EMBL: 249403; CAA89423.1; -  
 DR PIR: A32714; A32714.  
 DR SGD: S0003664; PBS2.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_AMP; FALSE\_NEG.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR TRANSFERASE: Serine/threonine-protein kinase; Tyrosine-protein kinase;  
 KW ATP-binding; Antibiotic resistance; Phosphorylation.  
 KW PRO-RICH.  
 FT DOMAIN 91 101  
 FT NP\_BIND 360 623  
 FT BINDING 366 374  
 FT ACT\_SITE 389 389  
 FT ACT\_SITE 485 485  
 FT MOD\_RES 514 514  
 FT MOD\_RES 518 518  
 FT MUTAGEN 96 96  
 FT MUTAGEN 389 389  
 FT MUTAGEN 514 514  
 FT MUTAGEN 518 518  
 FT CONFLICT 222 223  
 FT CONFLICT 222 223  
 FT CONFLICT 668 668  
 FT YIYICL (IN REF. 1).  
 SQ SEQUENCE 668 AA; 72719 MW; 9BC3435BDAFE8019 CMC64;  
 Query Match 35.0%; Score 606; DB 1; Length 668;  
 Best Local Similarity 37.3%; Pred. No. 2.9e-36;  
 Matches 141; Conservative 73; Mismatches 105; Indels 59; Gaps 12;  
 OY 4 KKKRRNGIKI-----PKKAFQPG-QTSSTPRRDSK----- 35  
 DB 265 EGRKRNPGSLINGVQSTSTSSSTGPHDYCTTPRTGNSNNSGSGGGLPFANFSQ 324  
 OY 36 ACISISGNQNF-----EVKADLPELIMELGRGAYGVEMKRRHVPSSGQ 76  
 DB 325 VDIKSGSLNFAGRKLSKSGKIDFSGSSSRITLDELPELDELGHGNYGNVSKVLRKPTNV 384

OY 77 IMAVKIRATVNSQEQRLMDLIDISMTKTVDCPFVTFYGLAFREGDVMICMLMD-TSL 135  
 DB 385 IMATKEVRLDEKDFKQIIMLELV-LHKNSPIVDYFGAFEEGAYVMEYDGGSL 443  
 OY 136 DKFYKQVIDKQGITIPEDILGKIVASYKALEHLHSLKSVIRPDVSPVNLNA-LGVYKM 194  
 DB 444 DKIDESSEIG-GIDEQLAFIANAVHIGLKELEOHNIHRDVPNILLCSANQGYKL 502  
 OY 195 CDGEGISGIVDSVAKTIDAGCKPYMAPERI--NPELNQKGYSAKSDIMSLGITMIELAI 251  
 DB 503 CDGEGSGNLVASLAKT-NIGQSYMAPERISLND--RAYTVGSDIMSLGITMIELAI 559  
 OY 252 LRFPPY-DSWGTPFQQLKQVVEEDSPQLPADKFAEYDFTSQCKKSKKEPTPELMO 309  
 DB 560 GRYPPEYTYDINFSQLSAIVDGPPIRPSDFSSDADPVSFLCKIIPRRPYAALTE 619  
 OY 310 HPFTLHESKGTDAASFV 327  
 DB 620 HPWLVKYRNQVHMSXYI 637  
 RESULT 13  
 MKFS\_RAT STANDARD: PRT: 448 AA.  
 AC 062862; Q62863; Q62864;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE dual specificity mitogen-activated protein kinase 5  
 DE (EC 2.7.1.-) (MAP kinase 5) (MAPK 5) (MAPK/ERK kinase 5).  
 GN MAP2K5 OR PRKMK5 OR MEK5 OR MKK5.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS.  
 RP STRAIN=Sprague-Dawley; TISSUE=brain;  
 RX MEDLINE=96081960; PubMed=7499418;  
 RA English J.M., Vanderbilt C.A., Xu S., Marcus S., Cobb M.H.;  
 RT "Isolation of MEK5 and differential expression of alternatively  
 RT spliced forms.";  
 RL J. Biol. Chem. 270:28897-28902(1995).  
 CC -1- FUNCTION: INTERACTS SPECIFICALLY WITH ERK5, AND NOT WITH OTHER MAP  
 CC KINASES SUCH AS ERK1, ERK2, ERK3, JNK/SAPK, OR P38. IS NOT  
 CC PHOSPHORYLATED BY RAF-1, C-MOS, OR MEK1.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (FOR MEK5-BETA) AND PARTICULATE  
 CC (MEK5-ALPHA). THE ALTERNATIVELY SPLICED EXON IN ALPHA ISOFORM  
 CC RESEMBLE CONSERVED SEQUENCES THAT MEDIATE INTERACTIONS WITH THE  
 CC CYTOSKELETON. THEREBY EXPLAINING THE DIFFERENTIAL LOCALIZATION.  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: ALPHA-1 (SHOWN HERE), ALPHA-  
 CC 2 AND BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: MEK5 BETA IS UNIDIRECTIONALLY DISTRIBUTED WITH  
 CC HIGHEST LEVELS IN THE LIVER, WHEREAS MEK5 ALPHA IS EXPRESSED ONLY  
 CC IN LIVER AND BRAIN.  
 CC -1- PTM: ACTIVATED BY PHOSPHORYLATION ON SER/THR BY MAP KINASE KINASE  
 CC KINASES (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U37462; AAC52320.1; -  
 DR EMBL: U37463; AAC52321.1; -  
 DR EMBL: U37464; AAC52322.1; -  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000270; Oetpept\_motif.



InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Pfam: PF00564; OPR; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00016; Burk\_pkinase; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;  
 KM ATP-binding; Phosphorylation; Alternative splicing.  
 FT DOMAIN 166 419  
 FT NP\_BIND 172 180  
 FT BINDING 193 195  
 FT ACT\_SITE 283 283  
 FT MOD\_RES 311 311  
 FT MOD\_RES 315 315  
 FT VARSPIC 349 358  
 FT VARSPIC 311 311  
 FT MUTAGEN 315 315  
 FT MOTAGEN 448 AA; 50197 MW; 1B1CC8B05789B90D CRC64;  
 SQ SEQUENCE

Query Match 33.9%; Score 587.5; DB 1; Length 448;  
 Best local similarity 42.7%; Pred. No. 3; Ee-35;  
 Matches 144; Conservative 53; Mismatches 111; Indels 29; Gaps 11;

5 GKRRNDGLKIPKAEFPQPTSTPPRDLDSKACISIGNQNFVKADLEPIHEL 58  
 113 GERINHGKVFTRAGSPQHSPTVSDSPENSLKSSAEELKILANQMEQDIRYDTL 172  
 59 GCGAVGVKMKRVBPGQIMAVKIRATVNSQDQKRLMDJISMRTVDFPTVFGAL 118  
 173 GCGNGGVKAVKAVHPGSKILAVVILLDTLELOKQIMSELELYCKDSSYLIGFGAF 231  
 119 FREGDWMIMELMDTSLDKEYQVIDKQGTPEIDIGKTAIVKALHSHKSLVYTHR 177  
 232 FVENRISICTEFMDGSLDYLR-----IPEHVLGRVAVVKKGLTFLMS-LKILHR 282  
 178 DVKPSNVLTALGVQVCKDVGISGLYVDVAKTIDAGCKPYMAPERINPELNQGYSVKS 237  
 283 DVKPSNMLVNTSGQVYLCDFGVSTQLVNSIAKTY-VGTNAYMAPERISGE---QYGIHS 337  
 238 DWSIGTMIETALIRFVY---DSWGT--PFQOLQVVEBPQPLADFFSAEFVDFTS 291  
 338 DWSIGTMIETALIRFVY---DSWGT--PFQOLQVVEBPQPLADFFSAEFVDFTS 291  
 292 QCLKNSKERPTYPPELMQHPFTT-LHESKGTDVASPV 327  
 398 QCMRKQKPERPAPEELMGHPTVQFMDGNATVYSMVV 434

RESULT 14  
 MPK1\_HUMAN STANDARD; PRT; 392 AA.  
 AC Q02750;  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Dual specifically mitogen-activated protein kinase kinase 1  
 DE (EC 2.7.1.-) (Map kinase kinase 1) (MEK1).  
 DE (MAPK/ERK kinase 1) (MEK1).  
 GN MAP2K1 OR PRKMK1 OR MEK1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RX MEDLINE=93100262; PubMed=1281467;  
 RA Seger R., Seger D., Lozeman F.J., Ahn N.G., Graves L.M.,  
 RA Campbell J.S., Ericsson L., Harrylock M., Jensen A.M., Krebs E.G.;  
 RT "Human T-cell mitogen-activated protein kinase kinases are related to  
 yeast signal transduction kinases.";

RL J. Biol. Chem. 267:25628-25631(1992).  
 RN [2]  
 RX MEDLINE=93266604; PubMed=8388392;  
 RA Zheng C.-F., Guan K.-L.;  
 RT "Cloning and characterization of two distinct human extracellular  
 signal-regulated kinase activator kinases, MEK1 and MEK2."  
 J. Biol. Chem. 268:11435-11439(1993).  
 RN [3]  
 RP PHOSPHORYLATION OF SER-217 AND SER-221, AND MUTAGENESIS.  
 RX MEDLINE=94178255; PubMed=8131746;  
 RA Zheng C.-F., Guan K.-L.;  
 RT "Activation of MEK family kinases requires phosphorylation of two  
 conserved Ser/Thr residues."  
 EMBO J. 13:1123-1131(1994).  
 RN [4]  
 RP CLEAVAGE BY ANTHRAX LETHAL FACTOR, AND SEQUENCE OF 8-16.  
 RX MEDLINE=98230732; PubMed=9563949;  
 RA Duesbery N.S., Webb C.P., Lepple S.H., Gordon V.M., Klimpel K.R.,  
 RA Copeland T.D., Ahn N.G., Oskarsson M.K., Fukasawa K., Paul K.D.,  
 RA Vande Woude G.F.;  
 RT "Proteolytic inactivation of MAP-kinase-kinase by anthrax lethal  
 factor."  
 Science 280:734-737(1998).  
 RN [5]  
 RP CLEAVAGE BY ANTHRAX LETHAL FACTOR.  
 RX MEDLINE=20558083; PubMed=11104681;  
 RA Vitale G., Bernardi L., Napolitani G., Mock M., Montecucco C.;  
 RT "Susceptibility of mitogen-activated protein kinase kinase family  
 members to proteolysis by anthrax lethal factor."  
 Biochem. J. 352:739-745(2000)  
 CC -1- FUNCTION: CATALYZES THE CONCOMITANT PHOSPHORYLATION OF A THREONINE  
 AND A TYROSINE RESIDUE IN A THR-GLU-TYR SEQUENCE LOCATED IN MAP  
 KINASES. ACTIVATES ERK1 AND ERK2 MAP KINASES.  
 CC -1- PTM: MAPK IS ITSELF DEPENDENT ON SER/THR PHOSPHORYLATION FOR  
 ACTIVITY CATALYZED BY MAP KINASE KINASE KINASES (RAF OR MEK1).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE SUBFAMILY.  
 CC CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: L05624; AAA36318.1;  
 CC EMBL: L11284; -; NOT\_ANNOTATED\_CDS.  
 CC PIR: A45100; A45100.  
 CC HSSP: 000534; 1B1F8.  
 CC Genew: HGNC:6840; MAP2K1.  
 CC MIM: 176872;  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;  
 KM ATP-binding; Phosphorylation.  
 FT INT\_MET 0  
 FT DOMAIN 0  
 FT NP\_BIND 67 360  
 FT BINDING 73 81  
 FT ACT\_SITE 96 96  
 FT MOD\_RES 189 189  
 FT MOD\_RES 217 217  
 FT MOD\_RES 221 221  
 FT DOMAIN 261 306  
 FT SITE 7 8  
 FT MOTAGEN 96 96  
 FT CLEAVAGE (BY ANTHRAX LETHAL FACTOR).  
 K->R: INACTIVATION.

FT MUTAGEN 149 149 S->A: NO LOSS OF ACTIVITY.  
 FT MUTAGEN 211 211 S->A: NO LOSS OF ACTIVITY.  
 FT MUTAGEN 217 217 S->A: INACTIVATION.  
 FT MUTAGEN 221 221 S->A: INACTIVATION.  
 SQ SEQUENCE 392 AA; 43307 MW; EF7194F7DA698734 CRC64;

Query Match 33.9%; Score 587; DB 1; Length 392;  
 Best Local Similarity 38.0%; Pred. No. 3.5e-35;  
 Matches 125; Conservative 62; Mismatches 90; Indels 52; Gaps 7;

QY 46 EVKADDDLEPIMELGAGVGVKMRHVPSCQIMAVKRIATVNSQEKRLMDLDSMRT 105  
 DB 61 ELKDDDFEKISELGANGNGVGVFKSHKSGVMAKRLHLEIKPAIRNOIIRLOV-LHE 119  
 QY 106 VDCPTVTYFALFREGDVMICMELMD-TSLDKFYQVYDKQGTIPEDILGKIVASIVA 164  
 DB 120 CNSPIYGVGAFYSDGEISICMEHMDGSLD---QVLKAGRIPEQLIGKIVASIVIG 175  
 QY 165 LEHLSKLSVTHRDVKKPSNVILNALGVKMGDFGISGVYDVAKTIDAGCKPYMAPERI 224  
 DB 176 LTYLREKHKIMHRDVKPSNVLNSKGEIKLCPFGVSGQLIDSMANSF-VGTRSYMSPER 233  
 QY 225 NPELNOKGYSVKSDIMSLGIMTEILALRPY-----DSMGRP----- 262  
 DB 234 ---LQGTHTSVQSDIMSMGLSLVEMAVGRYPIPPDAKELELMFCQVGEADAETPPRR 290  
 QY 263 -----FOOLKOVVEEPPSLPADKTSAEFVDFTSOCLKRNKSRPT 303  
 DB 291 TPGRPLSSYGMDSRPMAIFELLDYIVNEPPLPSGVSLERQDYEYVKKCLINPAPRAD 350  
 QY 304 YPELMOHPFTLHESKGTVDVASFVKILIG 332  
 DB 351 LKQIMVHAFIKRSDAEVDFAGWLCSTIG 379

RESULT 15  
 MK1 MOUSE STANDARD; PRT; 392 AA.  
 ID MK1 MOUSE  
 AC P31938;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Dual specificity mitogen-activated protein kinase kinase 1  
 DE (EC 2.7.1.-) (MAP kinase kinase 1) (MAPKK 1) (ERK activator kinase 1)  
 GN (MAPK/ERK kinase 1) (MEK1).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=93030761; PubMed=1411546;  
 RA Crews C.M., Alessandrini A., Erikson R.L.;  
 RT "The primary structure of MEK, a protein kinase that phosphorylates  
 RT the ERK gene product."  
 RL Science 258:478-480(1992).  
 RN [2]  
 RP SEQUENCE OF 3-19; 70-83; 113-135; 205-233 AND 362-383.  
 RC TISSUE="cell";  
 RX MEDLINE=92390415; PubMed=1381507;  
 RA Crews C.M., Erikson R.L.;  
 RT "Purification of a murine protein-tyrosine/threonine kinase that  
 RT phosphorylates and activates the Erk-1 gene product: relationship to  
 RT the fission yeast byr1 gene product."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:8205-8209(1992).  
 RN [3]  
 RP CLEAVAGE BY ANTHRAX LETHAL FACTOR.  
 RX MEDLINE=98230732; PubMed=9563949;  
 RA Duesberry N.S., Webb C.P., Leppia S.H., Gordon V.M., Klimpel K.R.,  
 RA Copeland T.D., Ahn N.G., Oskarsson M.K., Fukasawa K., Pauli K.D.,  
 RA Vande Woude G.F.;  
 RT "Proteolytic inactivation of MAP-kinase-kinase by anthrax lethal

RT factor.";  
 RL Science 280:734-737(1998).  
 CC -1- FUNCTION: CATALYZES THE CONCOMITANT PHOSPHORYLATION OF A THREONINE  
 CC AND A TYROSINE RESIDUE IN A THR-GLU-TYR SEQUENCE LOCATED IN MAP  
 CC KINASES. ACTIVATES ERK1 AND ERK2 MAP KINASES.  
 CC -1- ENZYME REGULATION: INHIBITED BY SERINE/THREONINE PHOSPHATASE 2 A.  
 CC -1- PTM: MAPK IS ITSELF DEPENDENT ON SER/THR PHOSPHORYLATION FOR  
 CC ACTIVITY CATALYZED BY MAP KINASE KINASE KINASES (RAF OR MEK1).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb.ch/announce/>  
 CC or send an email to [license@isb.ch](mailto:license@isb.ch)).  
 CC -----  
 CC EMBL: L02526; AAA39523.1; ..  
 CC HSP: Q00534; 1B18.  
 CC MGD: MGI:1346866; Map2K1.  
 CC InterPro: IPR000719; Euk\_Pkinase.  
 CC InterPro: IPR002290; Ser\_thr\_Pkinase.  
 CC Pfam: PF00065; Pkinase; 1.  
 CC ProDom: PD000001; Euk\_Pkinase; 1.  
 CC SMART: SM00220; S\_TKc; 1.  
 CC PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC DR transferase: Serine/threonine-protein kinase; Tyrosine-protein kinase;  
 CC KW ATP-binding; Phosphorylation.  
 CC FT INIT\_MET 0  
 CC FT DOMAIN 0  
 CC FT NP\_BIND 67 360  
 CC FT BINDING 73 81  
 CC FT ACT\_SITE 96 96  
 CC FT MOD\_RES 189 189  
 CC FT MOD\_RES 217 217  
 CC FT MOD\_RES 221 221  
 CC FT DOMAIN 261 306  
 CC FT SITE 7 8  
 CC FT CLEAVAGE (BY ANTHRAX LETHAL FACTOR) (BY  
 CC SIMILARITY).  
 CC FT PRO\_RICH  
 CC FT CONFLICT 373 373  
 CC SQ SEQUENCE 392 AA; 43343 MW; EDE454FD543EAB2 CRC64;  
 W -> Q (IN REF. 2).  
 Query Match 33.9%; Score 587; DB 1; Length 392;  
 Best Local Similarity 38.0%; Pred. No. 3.5e-35;  
 Matches 125; Conservative 62; Mismatches 90; Indels 52; Gaps 7;

QY 46 EVKADDDLEPIMELGAGVGVKMRHVPSCQIMAVKRIATVNSQEKRLMDLDSMRT 105  
 DB 61 ELKDDDFEKISELGANGNGVGVFKSHKSGVMAKRLHLEIKPAIRNOIIRLOV-LHE 119  
 QY 106 VDCPTVTYFALFREGDVMICMELMD-TSLDKFYQVYDKQGTIPEDILGKIVASIVA 164  
 DB 120 CNSPIYGVGAFYSDGEISICMEHMDGSLD---QVLKAGRIPEQLIGKIVASIVIG 175  
 QY 165 LEHLSKLSVTHRDVKKPSNVILNALGVKMGDFGISGVYDVAKTIDAGCKPYMAPERI 224  
 DB 176 LTYLREKHKIMHRDVKPSNVLNSKGEIKLCPFGVSGQLIDSMANSF-VGTRSYMSPER 233  
 QY 225 NPELNOKGYSVKSDIMSLGIMTEILALRPY-----DSMGRP----- 262  
 DB 234 ---LQGTHTSVQSDIMSMGLSLVEMAVGRYPIPPDAKELELMFCQVGEADAETPPRR 290  
 QY 263 -----FOOLKOVVEEPPSLPADKTSAEFVDFTSOCLKRNKSRPT 303  
 DB 291 TPGRPLSSYGMDSRPMAIFELLDYIVNEPPLPSGVSLERQDYEYVKKCLINPAPRAD 350  
 QY 304 YPELMOHPFTLHESKGTVDVASFVKILIG 332  
 DB 351 LKQIMVHAFIKRSDAEVDFAGWLCSTIG 379



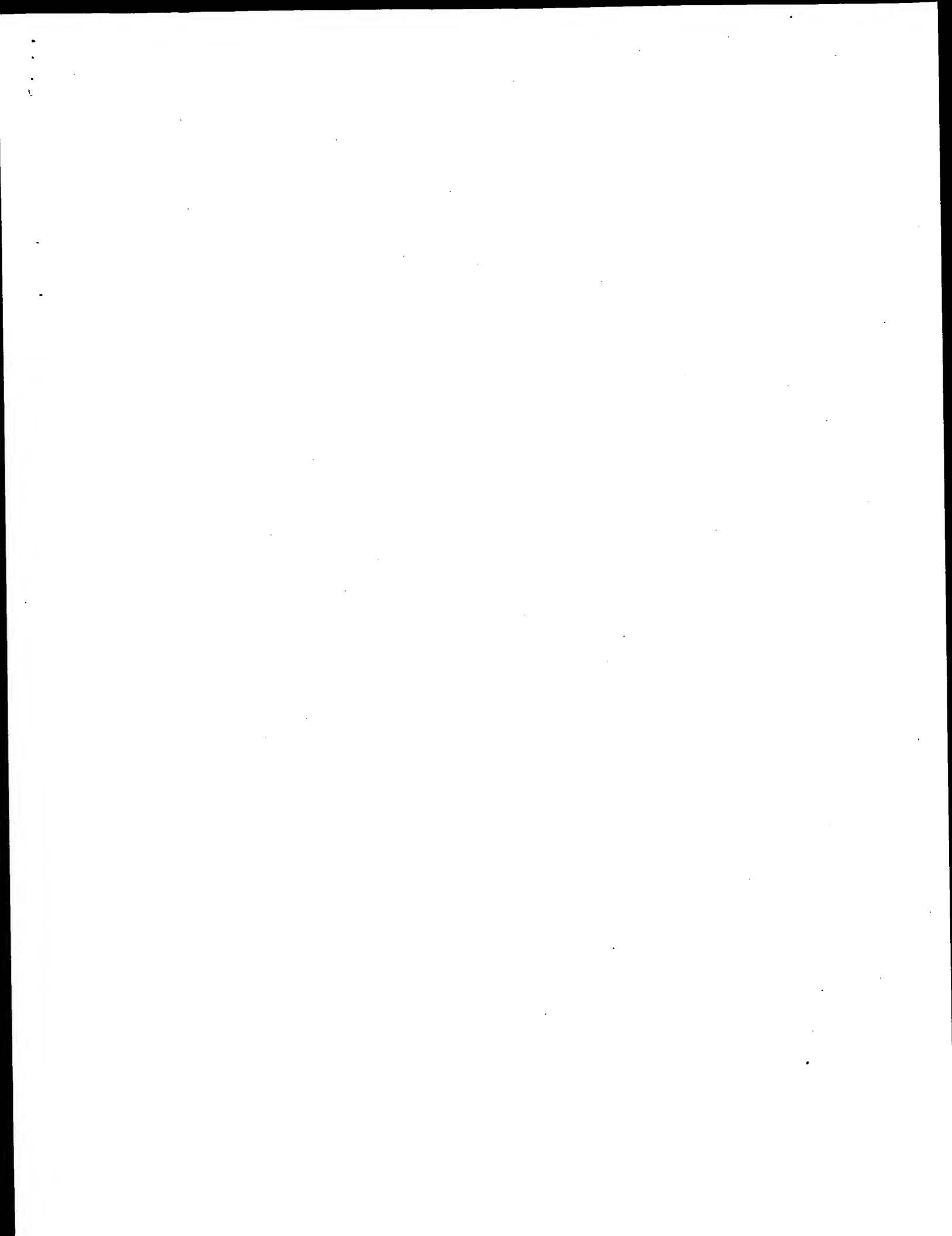
Fri Jun 6 15:36:19 2003

us-09-593-288-2.rsp

Page 13

Search completed: June 6, 2003, 09:10:47  
Job time : 13 secs

---



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2003, 09:05:58 ; Search time 32 Seconds

(without alignments)  
2144.178 Million cell updates/sec

Title: US-09-593-288-2

Perfect score: 1731  
Sequence: 1 SOSGKKRNPGLKIPKEAFE.....TLHESKGTDVASFVKLLIGD 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SPREMBL\_21:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organella:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*  
16: sp\_virus:\*  
17: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length | DB | ID     | Description             |
|------------|--------|-------------|--------|----|--------|-------------------------|
| 1          | 1699   | 98.2        | 334    | 11 | Q925D6 | Q925D6 rat mus musculus |
| 2          | 1583.5 | 91.5        | 335    | 13 | Q9PW48 | Q9PW48 xenopus lae      |
| 3          | 1523   | 88.0        | 404    | 13 | Q91959 | Q91959 cyprinus ca      |
| 4          | 1495.5 | 86.4        | 363    | 13 | Q9DGE0 | Q9DGE0 brachydanio      |
| 5          | 1384   | 80.0        | 347    | 4  | Q9UW72 | Q9UW72 homo sapien      |
| 6          | 1383   | 79.9        | 347    | 4  | Q9UW72 | Q9UW72 homo sapien      |
| 7          | 1370   | 79.1        | 347    | 11 | P97293 | P97293 mus musculus     |
| 8          | 1370   | 79.1        | 352    | 4  | Q9UW71 | Q9UW71 homo sapien      |
| 9          | 1221   | 70.5        | 237    | 11 | Q60521 | Q60521 mus musculus     |
| 10         | 1036   | 59.8        | 335    | 5  | Q9UW90 | Q9UW90 cyprinus ca      |
| 11         | 1034   | 59.7        | 334    | 5  | O62602 | O62602 drosophila       |
| 12         | 936.5  | 54.1        | 407    | 13 | Q8UW90 | Q8UW90 cyprinus ca      |
| 13         | 870.5  | 50.3        | 336    | 5  | Q95Y19 | Q95Y19 caenorhabdi      |
| 14         | 865.5  | 50.0        | 343    | 5  | Q21669 | Q21669 caenorhabdi      |
| 15         | 850    | 49.1        | 281    | 13 | Q9DGR7 | Q9DGR7 brachydanio      |
| 16         | 835.5  | 48.3        | 424    | 5  | O61444 | O61444 drosophila       |

|    |       |      |      |    |        |                     |
|----|-------|------|------|----|--------|---------------------|
| 17 | 822   | 47.5 | 162  | 11 | P70273 | P70273 mus musculus |
| 18 | 697.5 | 40.3 | 492  | 5  | O18411 | O18411 drosophila   |
| 19 | 697.5 | 40.3 | 1178 | 5  | O8S221 | O8S221 drosophila   |
| 20 | 694   | 40.1 | 389  | 11 | O35720 | O35720 mus musculus |
| 21 | 694   | 40.1 | 391  | 11 | O35872 | O35872 mus musculus |
| 22 | 694   | 40.1 | 419  | 11 | O35871 | O35871 mus musculus |
| 23 | 694   | 40.1 | 435  | 11 | O35871 | O35871 mus musculus |
| 24 | 694   | 40.1 | 468  | 11 | O54780 | O54780 mus musculus |
| 25 | 693.5 | 40.1 | 356  | 5  | O95U05 | O95U05 ancylostoma  |
| 26 | 692.5 | 40.0 | 417  | 13 | O8OHK7 | O8OHK7 xenopus lae  |
| 27 | 690.5 | 39.9 | 453  | 11 | O9R124 | O9R124 mus musculus |
| 28 | 690.5 | 39.9 | 459  | 11 | O9R126 | O9R126 mus musculus |
| 29 | 688.5 | 39.8 | 346  | 11 | O9QW66 | O9QW66 mus musculus |
| 30 | 685   | 39.6 | 380  | 11 | O9R123 | O9R123 mus musculus |
| 31 | 682.5 | 39.4 | 346  | 11 | O35406 | O35406 mus musculus |
| 32 | 618   | 35.7 | 359  | 5  | O01706 | O01706 caenorhabdi  |
| 33 | 610.5 | 35.3 | 505  | 5  | O21307 | O21307 caenorhabdi  |
| 34 | 588   | 34.0 | 400  | 11 | O91YS7 | O91YS7 mus musculus |
| 35 | 587.5 | 33.9 | 401  | 11 | O9D7B0 | O9D7B0 mus musculus |
| 36 | 587.5 | 33.9 | 448  | 11 | O9WVS7 | O9WVS7 mus musculus |
| 37 | 587   | 33.9 | 393  | 11 | O9JTE1 | O9JTE1 mus musculus |
| 38 | 584   | 33.7 | 448  | 4  | O92961 | O92961 mus musculus |
| 39 | 577   | 33.3 | 173  | 11 | O91YX1 | O91YX1 mus musculus |
| 40 | 575.5 | 33.2 | 683  | 3  | O96W50 | O96W50 debaromyce   |
| 41 | 575   | 33.2 | 393  | 6  | O9XT09 | O9XT09 pan troglod  |
| 42 | 564   | 32.6 | 371  | 5  | O23326 | O23326 caenorhabdi  |
| 43 | 563   | 32.5 | 397  | 13 | O8UW89 | O8UW89 cyprinus ca  |
| 44 | 553   | 31.9 | 451  | 4  | O92962 | O92962 homo sapien  |
| 45 | 542   | 31.3 | 396  | 5  | O9W360 | O9W360 drosophila   |

## ALIGNMENTS

| RESULT | ID     | Q925D6 | PRELIMINARY | PRT    | 334 AA. |
|--------|--------|--------|-------------|--------|---------|
| 1      | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 2      | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 3      | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 4      | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 5      | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 6      | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 7      | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 8      | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 9      | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 10     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 11     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 12     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 13     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 14     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 15     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 16     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 17     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 18     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 19     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 20     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 21     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 22     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 23     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 24     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 25     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 26     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 27     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 28     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 29     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 30     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 31     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 32     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 33     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 34     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 35     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 36     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 37     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 38     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 39     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 40     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 41     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 42     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 43     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 44     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |
| 45     | Q925D6 | Q925D6 | Q925D6      | Q925D6 | Q925D6  |

| Query Match | Score | Length | DB | ID     | Description             |
|-------------|-------|--------|----|--------|-------------------------|
| 1           | 98.2% | 334    | 11 | Q925D6 | Q925D6 rat mus musculus |
| 2           | 91.5% | 335    | 13 | Q9PW48 | Q9PW48 xenopus lae      |
| 3           | 88.0% | 404    | 13 | Q91959 | Q91959 cyprinus ca      |
| 4           | 86.4% | 363    | 13 | Q9DGE0 | Q9DGE0 brachydanio      |
| 5           | 80.0% | 347    | 4  | Q9UW72 | Q9UW72 homo sapien      |
| 6           | 79.9% | 347    | 4  | Q9UW72 | Q9UW72 homo sapien      |
| 7           | 79.1% | 347    | 11 | P97293 | P97293 mus musculus     |
| 8           | 79.1% | 352    | 4  | Q9UW71 | Q9UW71 homo sapien      |
| 9           | 70.5% | 237    | 11 | Q60521 | Q60521 mus musculus     |
| 10          | 59.8% | 335    | 5  | Q9UW90 | Q9UW90 cyprinus ca      |
| 11          | 59.7% | 334    | 5  | O62602 | O62602 drosophila       |
| 12          | 54.1% | 407    | 13 | Q8UW90 | Q8UW90 cyprinus ca      |
| 13          | 50.3% | 336    | 5  | Q95Y19 | Q95Y19 caenorhabdi      |
| 14          | 50.0% | 343    | 5  | Q21669 | Q21669 caenorhabdi      |
| 15          | 49.1% | 281    | 13 | Q9DGR7 | Q9DGR7 brachydanio      |
| 16          | 48.3% | 424    | 5  | O61444 | O61444 drosophila       |

QY 61 GAYGVEKMRHVPSSQIMAVKRIKIRATVNSQEQKRLMDIDISMRTVDCPFTVTFYGLFR 120  
 DB 62 GAYGVEKMRHVPSSQIMAVKRIKIRATVNSQEQKRLMDIDISMRTVDCPFTVTFYGLFR 121  
 QY 121 EGDVWICMELMDTSLDKFYKQVYIDKQGTIPEDILKINAVSIVKALEHLSKLSVIRHDVK 180  
 DB 122 EGDVWICMELMDTSLDKFYKQVYIDKQGTIPEDILKINAVSIVKALEHLSKLSVIRHDVK 181  
 QY 181 PSNVILNALGOVKMCDFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVSKDIW 240  
 DB 182 PSNVILNALGOVKMCDFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVSKDIW 241  
 QY 241 SLGITMIELAILRFPYDSWGTTPFOOLKQVVEEPPSLPADKFSAEFVDFTSQCLKRNKSK 300  
 DB 242 SLGITMIELAILRFPYDSWGTTPFOOLKQVVEEPPSLPADKFSAEFVDFTSQCLKRNKSK 301  
 QY 301 RPTYPELMOHPEFTLHESKGTDVASFVKLILGD 333  
 DB 302 RPTYPELMOHPEFTLHESKGTDVASFVKLILGD 334

## RESULT 2

Q9PW48 PRELIMINARY: PRT: 335 AA.  
 ID 09PW48: PRELIMINARY: PRT: 335 AA.  
 AC 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE MAP kinase activator XMEK3.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8335;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20065138; Pubmed=10597270;  
 RA Kieran M.W., Katz S., Vail B., Zon L.I., Mayer B.J.;  
 RT "Concentration-dependent positive and negative regulation of a MAP  
 RT kinase by a MAP kinase kinase."  
 RL Oncogene 18:6647-6657(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Kieran M., Vail B., Zon L.I., Mayer B.J.;  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL: AF172848; AAD9421.1; -  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase: 1.  
 DR ProDom: PD000001; Euk\_pkinase: 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR KAP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 KW SEQUENCE 335 AA; 37923 MW; 29369A6D25B4DB57 CRC64;

Query Match 91.5%; Score 1583.5; DB 13; Length 335;  
 Best Local Similarity 92.2%; Pred. No. 3.6e-128;  
 Matches 308; Conservative 8; Mismatches 17; Indels 1; Gaps 1;

QY 1 SOSKGRKRNPKLIPKEAFEPQTS-TPPRDLDSKACISIGNONFEVAKADLEPIELG 59  
 DB 2 SQARGKRNKRGKIPKEAFEPQTS-TPPRDLDSKACISIGNONFEVAKADLEPIELG 61  
 QY 60 RGAGVEKMRHVPSSQIMAVKRIKIRATVNSQEQKRLMDIDISMRTVDCPFTVTFYGLFR 119  
 DB 62 RGAGVEKMRHVPSSQIMAVKRIKIRATVNSQEQKRLMDIDISMRTVDCPFTVTFYGLFR 121  
 QY 120 REGDVWICMELMDTSLDKFYKQVYIDKQGTIPEDILKINAVSIVKALEHLSKLSVIRHDV 179  
 DB 122 REGDVWICMELMDTSLDKFYKQVYIDKQGTIPEDILKINAVSIVKALEHLSKLSVIRHDV 181

QY 180 KPSNVILNALGOVKMCDFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVSKDI 239  
 DB 182 KPSNVILNALGOVKMCDFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVSKDI 241  
 QY 240 WSLGITMIELAILRFPYDSWGTTPFOOLKQVVEEPPSLPADKFSAEFVDFTSQCLKRNKSK 299  
 DB 242 WSLGITMIELAILRFPYDSWGTTPFOOLKQVVEEPPSLPADKFSAEFVDFTSQCLKRNKSK 301  
 QY 300 ERTYPELMOHPEFTLHESKGTDVASFVKLILGD 333  
 DB 302 ERTYPELMOHPEFTLHESKGTDVASFVKLILGD 335

## RESULT 3

Q91959 PRELIMINARY: PRT: 404 AA.  
 ID 091959: PRELIMINARY: PRT: 404 AA.  
 AC 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE MAP kinase kinase 6 (MKK6).  
 OS Cyprinus carpio (Common carp).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Cyprinus.  
 OX NCBI\_TaxID=7962;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hashimoto H.;  
 RT "p38 MAPK cascade in fish."  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL: AB023480; BAA96414.1; -  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase: 1.  
 DR ProDom: PD000001; Euk\_pkinase: 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 KW SEQUENCE 404 AA; 45370 MW; 698435FE24057059 CRC64;

Query Match 88.0%; Score 1523; DB 13; Length 404;  
 Best Local Similarity 87.1%; Pred. No. 7.5e-123;  
 Matches 290; Conservative 20; Mismatches 23; Indels 0; Gaps 0;

QY 1 SOSKGRKRNPKLIPKEAFEPQTS-TPPRDLDSKACISIGNONFEVAKADLEPIELG 60  
 DB 72 SNKAGKRNKRGKIPKEAFEPQTS-TPPRDLDSKACISIGNONFEVAKADLEPIELG 131  
 QY 61 GAYGVEKMRHVPSSQIMAVKRIKIRATVNSQEQKRLMDIDISMRTVDCPFTVTFYGLFR 120  
 DB 132 GAYGVEKMRHVPSSQIMAVKRIKIRATVNSQEQKRLMDIDISMRTVDCPFTVTFYGLFR 191  
 QY 121 EGDVWICMELMDTSLDKFYKQVYIDKQGTIPEDILKINAVSIVKALEHLSKLSVIRHDVK 180  
 DB 192 EGDVWICMELMDTSLDKFYKQVYIDKQGTIPEDILKINAVSIVKALEHLSKLSVIRHDVK 251  
 QY 181 PSNVILNALGOVKMCDFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVSKDIW 240  
 DB 252 PSNVILNALGOVKMCDFGISGYLVDSVAKTIDAGCKPYMAPERINPELNOKGYSVSKDIW 311  
 QY 241 SLGITMIELAILRFPYDSWGTTPFOOLKQVVEEPPSLPADKFSAEFVDFTSQCLKRNKSK 300  
 DB 312 SLGITMIELAILRFPYDSWGTTPFOOLKQVVEEPPSLPADKFSAEFVDFTSQCLKRNKSK 371  
 QY 301 RPTYPELMOHPEFTLHESKGTDVASFVKLILGD 333  
 DB 372 RPTYPELMOHPEFTLHESKGTDVASFVKLILGD 404

## RESULT 4

Q9DGEO

ID 09DGE0 PRELIMINARY; PRT; 363 AA.  
 AC 09DGE0;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE MKK3.  
 GN MAP2K3 OR ZMKK3.  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 CC Cyprinidae; Danio.  
 NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20451058; PubMed=10995439;  
 RA Fujii R., Yamashita S., Hibi M., Hirano T.;  
 RT "Asymmetric p38 Activation in Zebrafish: Its Possible Role in  
 RT Symmetric and Synchronous Cleavage";  
 RL J. Cell Biol. 150:1335-1348(2000).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AB030899; BAB11809.1; -;  
 DR ZFIN; ZDB-GENE-010202-3; map2k3.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Prodom; PD000001; Euk\_pkinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Serine/threonine-protein kinase; Transferase;  
 SQ SEQUENCE 363 AA; 40807 MW; 02A7CD9A6F5A2DC CRC64;

Query Match 86.4%; Score 1495.5; DB 13; Length 363;  
 Best Local Similarity 87.0%; Pred. No. 1.5e-120;  
 Matches 288; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

QY 4 KGRKRP-GLKIPKEAFEPOTSSTPRDLSKACISIGNONFEVKADLEPIMELGR 62  
 DB 33 ROKKRIPEKELKPEKFEKAPAPPTPRDLSKAYVTIGENFVKKADLEIGELGR 92  
 QY 63 YGVVERKMRHVPSCQINAVKRIRATVNSQEQRLMDIDISRTYDCPTVFYGFALFR 122  
 DB 93 YGVVDRMRHVPSCQINAVKRIRATVNTQEQRLMDIDISRTYDCPTVFYGFALFR 152  
 QY 123 DWIMICELMDTSLDKRYKQYIDKGOTIPEDILGKINAVKALHLSKLSYIHRDVK 182  
 DB 153 DWIMICELMDTSLDKRYKQYIDKGOTIPEDILGKITVSIKALEHLSNLSYIHRDVK 212  
 QY 183 NVLINAGVKKMDFGISGYLVDSVAKTIDAGCKPYAPERINPELNOKGYSKSDIWSL 242  
 DB 213 NVLINAGVKKMDFGISGYLVDSVAKTIDAGCKPYAPERINPELNOKGYSKSDIWSL 272  
 QY 243 GITMIELALIRPYDSMGTPFPQOLKQVVEPSPOLPADKFSAEVDFTSQCLKKNSKE 302  
 DB 273 GITMIELALIRPYDSMGTPFPQOLKQVVEPSPOLPADKFSAEVDFTSQCLKKNSKE 332  
 QY 303 TYPBELMQHPFTLHESKGTVDVASFVKILID 333  
 DB 333 TYPBELMQHPFTLHESKGTVDVASFVKILID 363

## RESULT 5

Q9UE72 PRELIMINARY; PRT; 347 AA.  
 AC 09UE72;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE MAP kinase 3b.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Han Jiahua;  
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; U66839; ABA0652.1; -;  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Prodom; PD000001; Euk\_pkinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 347 AA; 39317 MW; A80BA4FDF8F7D82 CRC64;

Query Match 80.0%; Score 1384; DB 4; Length 347;  
 Best Local Similarity 80.2%; Pred. No. 5.7e-111;  
 Matches 267; Conservative 33; Mismatches 31; Indels 2; Gaps 2;

QY 2 QSKCK-KRNPGLKIPKEAFEPOTSSTPRDLSKACISIGNONFEVKADLEPIMELGR 60  
 DB 14 QSKCKSKKKKDLRISCMS-KPPAPPTPRDLSKAYVTIGENFVKKADLEIGELGR 72  
 QY 61 GAYVVERKMRHVPSCQINAVKRIRATVNSQEQRLMDIDISRTYDCPTVFYGFALFR 120  
 DB 73 GAYVVERKMRHVPSCQINAVKRIRATVNSQEQRLMDIDISRTYDCPTVFYGFALFR 132  
 QY 121 EGDWIMICELMDTSLDKRYKQYIDKGOTIPEDILGKINAVKALHLSKLSYIHRDVK 180  
 DB 133 EGDWIMICELMDTSLDKRYKQYIDKGOTIPEDILGKINAVKALHLSKLSYIHRDVK 192  
 QY 181 PSNVLINAGVKKMDFGISGYLVDSVAKTIDAGCKPYAPERINPELNOKGYSKSDIWSL 240  
 DB 193 PSNVLINAGVKKMDFGISGYLVDSVAKTIDAGCKPYAPERINPELNOKGYSKSDIWSL 252  
 QY 241 SLGITMIELALIRPYDSMGTPFPQOLKQVVEPSPOLPADKFSAEVDFTSQCLKKNSKE 300  
 DB 253 SLGITMIELALIRPYDSMGTPFPQOLKQVVEPSPOLPADKFSAEVDFTSQCLKKNSKE 312  
 QY 301 RPTYPELMQHPFTLHESKGTVDVASFVKILID 333  
 DB 313 RPTYPELMQHPFTLHESKGTVDVASFVKILID 345

## RESULT 6

Q99441 PRELIMINARY; PRT; 347 AA.  
 AC 099441;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE MAP kinase kinase 3b.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Moriguchi T., Toyoshima F., Gotoh Y., Iwamatsu A., Irie K., Mori E.,  
 RA Kuroyanagi N., Hagiwara M., Matsumoto K., Nishida E.;  
 RT "Purification and Identification of a major activator for p38 from  
 RT osmotically shocked cells. Activation of MAPK6 by osmotic shock,  
 RT tumor necrosis factor-alpha and H2O2.";  
 RL J. Biol. Chem. 0:0-0(1996).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9705154; PubMed=8900184;  
 RA Moriguchi T., Toyoshima F., Gotoh Y., Iwamatsu A., Irie K., Mori E.,  
 RA Kuroyanagi N., Hagiwara M., Matsumoto K., Nishida E.;



RESULT 8

Q9UE71 PRELIMINARY: PRT; 352 AA.

AC Q9UE71: 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

DE MAP kinase 3c.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCB1\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Han Jiahui;

RT Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL: U06840; AAB40653.1; -

DR InterPro: IPR000719; Euk\_pkinase.

DR InterPro: IPR002290; Ser\_thr\_pkinase.

DR Pfam: PF000069; Pkinase; 1.

DR ProDom: PD000001; Euk\_pkinase; 1.

DR SMART: SM00220; S\_TKC; 1.

DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.

DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SO SEQUENCE 352 AA; 39939 MW; F59612D9001E1E5 CRC64;

Query Match

Best Local Similarity 79.18; Score 1370; DB 4; Length 352;

Matches 264; Conservative 33; Mismatches 31; Indels 2; Gaps 2;

QY 5 GK-KRNPGLIKPKAFEPQSSPPRPDLDSKACISIGNONPEYKADLEPIEMELGRAY 63

DB 22 GKSKRRKDLKISCMS-KRPADNPPIPRNLDLSRTITIGDRNEFEADLVVISLGRGAY 80

QY 64 GVEEKNRHPVSGOIMAVKRIATVNSOEOKRLMDLDSMTVPCPEFTVTFYGAFFREGD 123

DB 81 GVEEKNRHPVSGOIMAVKRIATVNSOEOKRLMDLDSMTVPCPEFTVTFYGAFFREGD 140

QY 124 VVICMELMDTSLDKFYQVVDKGTIPEDILGKTAIVSLKALEHLSKLSVYHRDKPSN 183

DB 141 VVICMELMDTSLDKFYQVVDKGTIPEDILGKTAIVSLKALEHLSKLSVYHRDKPSN 200

QY 184 VVICMELMDTSLDKFYQVVDKGTIPEDILGKTAIVSLKALEHLSKLSVYHRDKPSN 243

DB 201 VVICMELMDTSLDKFYQVVDKGTIPEDILGKTAIVSLKALEHLSKLSVYHRDKPSN 260

QY 244 VVICMELMDTSLDKFYQVVDKGTIPEDILGKTAIVSLKALEHLSKLSVYHRDKPSN 303

DB 261 VVICMELMDTSLDKFYQVVDKGTIPEDILGKTAIVSLKALEHLSKLSVYHRDKPSN 320

QY 304 VVICMELMDTSLDKFYQVVDKGTIPEDILGKTAIVSLKALEHLSKLSVYHRDKPSN 330

DB 321 VVICMELMDTSLDKFYQVVDKGTIPEDILGKTAIVSLKALEHLSKLSVYHRDKPSN 350

RESULT 9

Q60521 PRELIMINARY: PRT; 237 AA.

AC Q60521: 01-NOV-1996 (Tremblrel. 01, Created)

DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

DE MAP kinase 6c.

GN MAPK6.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCB1\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=96216353; PubMed=8621675;

RT "Characterization of the structure and function of a novel MAP kinase (MKK6)."

RT Kinase (MKK6)."

RL J. Biol. Chem. 271:2886-2891(1996).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL: U39066; AAB03709.1; -

DR MGI: MGI:1346870; Map2k6.

DR InterPro: IPR000719; Euk\_pkinase.

DR InterPro: IPR002290; Ser\_thr\_pkinase.

DR Pfam: PF000069; Pkinase; 1.

DR ProDom: PD000001; Euk\_pkinase; 1.

DR PROSITE: PS50011; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.

DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SO SEQUENCE 237 AA; 26691 MW; 17D945B25D908B45 CRC64;

Query Match

Best Local Similarity 70.58; Score 1221; DB 11; Length 237;

Matches 231; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 97 MDLDSKRTVDCPEFTVTFYGAFFREGDVCICMELMDTSLDKFYQVVDKGTIPEDILGK 156

DB 1 MDLDSKRTVDCPEFTVTFYGAFFREGDVCICMELMDTSLDKFYQVVDKGTIPEDILGK 60

QY 157 IAVSIKALEHLSKLSVYHRDKPSNVLLNALGOVMKCPDGISGYLVDSYAKTIDAGCK 216

DB 61 IAVSIKALEHLSKLSVYHRDKPSNVLLNALGOVMKCPDGISGYLVDSYAKTIDAGCK 120

QY 217 PYMAPKINELNOKGYSVSDIWSLGTITMELAILRPYDSWGTTPQOLKQVVEEPPQ 276

DB 121 PYMAPKINELNOKGYSVSDIWSLGTITMELAILRPYDSWGTTPQOLKQVVEEPPQ 180

QY 277 LPADKSAEFTVDSOCLKNSKERPPYPELMOHPFTLHESKADVASFKLLIGD 333

DB 181 LPADKSAEFTVDSOCLKNSKERPPYPELMOHPFTLHESKADVASFKLLIGD 237

RESULT 10

Q9U983 PRELIMINARY: PRT; 335 AA.

AC Q9U983: 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

DE MAPK.

GN LIC OR LICORNE OR CG12244.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCB1\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=99292686; PubMed=10364162;

RT Suzanne M., Title K., Glise B., Agnes F., Mori E., Matsumoto K., Noselli S.

RT "The Drosophila p38 MAPK pathway is required during oogenesis for egg asymmetric development."

CC Genes Dev. 13:1464-1474(1999).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL: AJ238572; CAB45101.1; -

DR Flybase: FBgn0015763; IIC.

DR InterPro: IPR000719; Euk\_pkinase.

DR InterPro: IPR002290; Ser\_thr\_pkinase.

DR Pfam: PF000069; Pkinase; 1.

DR ProDom: PD000001; Euk\_pkinase; 1.

DR PROSITE: PS50011; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.

DR ATP-binding; Serine/threonine-protein kinase; Transferase.

SO SEQUENCE 335 AA; 38195 MW; FD31CA66ECB95F1BE CRC64;





QY 320 GIDVASFVKIL 331  
 Db 314 NFDISEFVARIL 325

## RESULT 12

Q80W90 PRELIMINARY; PRT; 407 AA.  
 AC 080W90;  
 DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE MAP kinase kinase 4.  
 GN CMK4.  
 OS Cyprinus carpio (Common carp).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Cyprinus.  
 OX NCBI\_Taxid=7962;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hashimoto H.;  
 RT "Carp MKK4";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB063389; BAB79524.1;  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Prodom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR SMART: SM00219; Tyrc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; UNKNOWN\_1.  
 KW kinase.  
 SQ SEQUENCE 407 AA; 46091 MW; 3A178B6C24867CCB CRC64;

## Query Match

Best Local Similarity 54.1%; Score 936.5; DB 13; Length 407;  
 Matches 185; Conservative 56; Mismatches 88; Indels 27; Gaps 6;

QY 2 OSKGRK-----NPKLK-----IPKEAFEPQTSSTPRDLDSKACISIG- 41  
 Db 43 OSDSGKRAKLKLNFPANPPIKPTSRITLNTAGLP---FQNPHERLRTSHIESGKLIKSP 99  
 QY 42 NONFEVKAADLEPIIMELGKAYGVYKMRHVPSSGOIMAYKRTATYNSQOKRLMDLDI 101  
 Db 100 EQHMDFTADLKDLEIGKAYGSVKNVHAKFSGOIMAYKRTATYNSQOKRLMDLDV 159  
 QY 102 SMRTVDCPFTVTFYGALEFREGDVTICMELMDTSLDKFYKQVIDK-GQITPEDILGKIAVS 160  
 Db 160 VMRSDDCPYIVQYFALFREGDVTICMELMDTSLDKFYKQVIDK-GQITPEDILGKIAVS 219  
 QY 161 IVKALEHSHKLSVHRDVKPSNVILNALGOVKMCDFGISGLYVDSVAKTIDAGCKPYMA 220  
 Db 220 TVKALNHLKEMKIKTHIDKIPSNILDLRKNIKILDFGISGLYVDSVAKTIDAGCKPYMA 279  
 QY 221 PERINPELNOKGYSVKSDIMSLGIMIELALIRFPYDSGTPPOOLKOVEEESPOLPAD 280  
 Db 280 PERIDPSASRGQYDRSDVMSIGITLYELATGRFPYKPNASVFDOLTVQVKGDPOLSSS 339  
 QY 281 ---KFAEFVDFTSOCLKKNKSRPTYPELMOHPEFTLHESKGTVDVASFVKILIGD 333  
 Db 340 EERQFSKFINFVNLCITKESKRPKYLKHPFIQWMEERTVDVASFVKILIDE 395

## RESULT 13

Q95Y19 PRELIMINARY; PRT; 336 AA.  
 AC Q95Y19;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE MAP kinase kinase SEK-1.  
 GN SEK-1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_Taxid=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tanaka-Hino M., Sagasti A., Hisamoto N., Kawasaki M., Nakano S.,  
 RA Ninomiya-Tsuji J., Bargmann C.I., Matsumoto K.;  
 RT "Cakml1-p38/MAPK pathway that determines neuronal asymmetric  
 development in C.elegans";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB060731; BAB43977.2;  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Prodom: PD000001; Euk\_pkinase; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; UNKNOWN\_1.  
 KW ATP-binding; Kinase; Transferase.  
 SQ SEQUENCE 336 AA; 38700 MW; 5E5E4EE1CC374FA0 CRC64;

## Query Match

Best Local Similarity 50.3%; Score 870.5; DB 5; Length 336;  
 Matches 170; Conservative 64; Mismatches 90; Indels 11; Gaps 6;

QY 2 OSKGRKRN-PGLKIRKEAFEPQTSSTPRDLDSKACISIGNON--FEVKADLEPIIMEL 58  
 Db 2 ERKGRKRLPKMKI-----VMPTVETTPMNLDRCLIKLNESEEIEIAATLVYLEEL 56  
 QY 59 GRGAYGVYKMRHVPSSGOIMAYKRTATYNSQOKRLMDLDISMTVDCPFTVTFYGALE 118  
 Db 57 GKGYGVYKMRHVPSSGOIMAYKRTATYNSQOKRLMDLDISMTVDCPFTVTFYGALE 116  
 QY 119 FREGDVTICMELMDTSLDKFYKQVIDKQITPEDILGKIAVSIVKALEHSHKLSVYIHRD 178  
 Db 117 FREGDVTICMELMDTSLDKFYKQVIDKQITPEDILGKIAVSIVKALEHSHKLSVYIHRD 176  
 QY 179 VKPSNVILNALGOVKMCDFGISGLYVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSD 238  
 Db 177 VKPSNVILNALGOVKMCDFGISGLYVDSVAKTIDAGCKPYMAPERINPELNOKGYSVKSD 235  
 QY 239 IWSLIGITMIELALIRFPYDSGTPPOOLKOVEEESPOLPADK-FSAEFVDFTSOCLKKN 297  
 Db 236 VWSLIGITMIELALIRFPYDSGTPPOOLKOVEEESPOLPADK-FSAEFVDFTSOCLKKN 295  
 QY 298 SKERTYPELMOHPEFTLHESKGTVDVASFVKIL 331  
 Db 296 YNERPKYPELMAMPMEQARNEKPSMAFNEIL 330

## RESULT 14

Q21669 PRELIMINARY; PRT; 343 AA.  
 AC Q21669;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE R03G5.2 protein.  
 GN R03G5.2.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_Taxid=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=94150718; Pubmed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

